


APPENDIX A

BLAST

Basic Local Alignment Search Tool

[Edit](#) and [Resubmit](#) [Save Search](#) [Strategies](#) [Formatting options](#) [Explain](#)

SEQID40

Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

*|25193

ic|25193

Description

SEQID40

Molecule type

amino acid

Query Length

597

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.24+ Citation

References

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Reference : [compositional analysis results report](#)

Stephen F. Altschul, John C. Woitton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#)

Search Parameters

Search parameter name Search parameter value

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Database

Database parameter name Database parameter value

Posted date	Sep 26, 2010 5:43 PM
Number of letters	4,071,357,309
Number of sequences	11,921,515
Entrez query	none

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.318492	0.267
K	0.132452	0.041
H	0.386991	0.14

Results Statistics

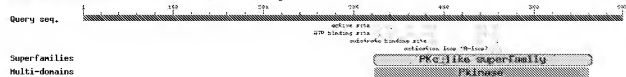
Results Statistics parameter name Results Statistics parameter value

Length adjustment	144
Effective length of query	453
Effective length of database	2354659149
Effective search space	1066660594497
Effective search space used	1066660594497

Graphic Summary

Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



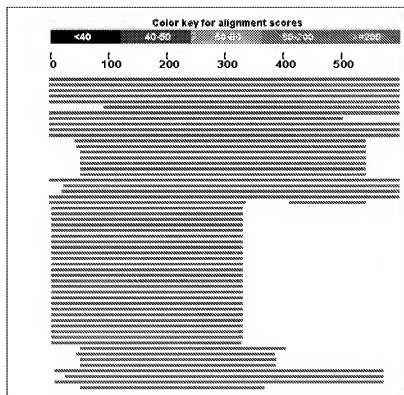
Super-families

Multi-domains

Distribution of 102 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer PubChem BioAssay
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
AB018960.1	NFR5a [Glycine max] >g ADJ19105.1 Nod-factor receptor 5A [Glycine max] >g ADJ19108.1 Nod-factor receptor 5A [Glycine max]	1058	1058	100%	0.0	
AD11891.1	Nod-factor receptor 5A [Glycine max]	1057	1057	100%	0.0	G
AD119102.1	Nod-factor receptor 5A [Glycine max]	1058	1055	100%	0.0	G
AG19112.1	Nod-factor receptor 5B [Glycine max]	1059	1029	100%	0.0	G
AD119111.1	Nod-factor receptor 5B [Glycine max]	1028	1028	100%	0.0	G
AB029613.1	NFR5b [Glycine max]	939	909	84%	0.0	
CAE02594.1	SYM10 protein [Pisum sativum] >emb CAE02594.1 SYM10 protein [Pisum sativum]	870	870	100%	0.0	
AD119110.1	truncated Nod-factor receptor 5A [Glycine max]	868	866	83%	0.0	G
CAE02595.1	SYM10 protein [Pisum sativum] >emb CAE02596.1 SYM10 protein [Pisum sativum] >g ADB5277.1 Nod factor recognition protein [Pisum sativum]	869	865	100%	0.0	
CAE02987.1	Nod-factor receptor 5 [Lotus japonicus] >emb CAE02598.1 Nod-factor receptor 5 [Lotus japonicus]	862	862	100%	0.0	G
ABF10224.1	Nod factor perception protein [Medicago truncatula]	802	839	100%	0.0	
CA002958.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	740	740	83%	0.0	
CA002959.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	733	733	82%	0.0	
CA002959.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02934.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02935.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02938.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02939.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02952.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02959.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02967.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02971.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02972.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02973.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	725	725	81%	0.0	
	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	722	723	81%	0.0	
	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	723	723	81%	0.0	
	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02970.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	722	722	81%	0.0	
	LysM-domain containing receptor-like kinase [Medicago tomatia]	718	718	81%	0.0	
	LysM type receptor kinase [Lotus japonicus] >dbj BAI79285.1 LysM type receptor kinase [Lotus japonicus]	706	706	100%	0.0	G
	PREDICTED: hypothetical protein [Xis virifer] >emb CBH17584.3 unnamed protein product [Xis virifer]	643	643	95%	0.0	G
	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >g EEF29112.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	618	618	96%	6e-175	
	predicted protein [Populus trichocarpa] >g EEE00646.1 predicted protein [Populus trichocarpa]	594	595	100%	7e-168	G
	truncated Nod-factor receptor 5A [Glycine max]	536	536	56%	4e-150	G
BA080147.1	Nod factor receptor protein [Glycine max]	519	519	54%	4e-145	
BA080149.1	Nod factor receptor protein [Glycine soja] >dbj BA085149.1 Nod factor receptor protein [Glycine soja] >dbj BA085150.1 Nod factor receptor protein [Glycine max] >dbj BA085160.1 Nod factor receptor protein [Glycine max] >dbj BA085161.1 Nod factor receptor protein [Glycine max] >dbj BA085162.1 Nod factor receptor protein [Glycine max] >dbj BA085165.1 Nod factor receptor protein [Glycine max] >dbj BA085166.1 Nod factor receptor protein [Glycine max] >dbj BA085171.1 Nod factor receptor protein [Glycine max] >dbj BA085174.1 Nod factor receptor protein [Glycine max] >dbj BA085177.1 Nod factor receptor protein [Glycine max] >dbj BA085179.1 Nod factor receptor protein [Glycine max] >dbj BA085180.1 Nod factor receptor protein [Glycine max]	516	516	54%	3e-144	
	Nod factor receptor protein [Glycine soja]	516	516	54%	5e-144	
	Nod factor receptor protein [Glycine soja]	516	515	54%	5e-144	
	Nod factor receptor protein [Glycine max]	516	514	54%	9e-144	G
	Nod factor receptor protein [Glycine soja] >dbj BA085145.1 Nod factor receptor protein [Glycine soja]	514	514	54%	1e-143	
	Nod factor receptor protein [Glycine max]	516	514	54%	1e-143	
	Nod factor receptor protein [Glycine max]	514	514	54%	1e-143	
	Nod factor receptor protein [Glycine max]	515	514	54%	1e-143	
	Nod factor receptor protein [Glycine soja]	515	514	54%	1e-143	
	Nod factor receptor protein [Glycine soja]	514	514	54%	1e-143	

BAG88150.1	Nod factor receptor protein [Glycine soja]	516	514	54%	2e-143
BAG88158.1	Nod factor receptor protein [Glycine max]	514	514	54%	2e-143 G
BAG88172.1	Nod factor receptor protein [Glycine max]	514	514	54%	2e-143
BAG88162.1	Nod factor receptor protein [Glycine soja]	513	513	54%	2e-143
BAG88175.1	Nod factor receptor protein [Glycine max]	513	513	54%	3e-143
BAG88180.1	Nod factor receptor protein [Glycine soja]	512	513	54%	3e-143
BAG88173.1	Nod factor receptor protein [Glycine max]	513	513	54%	3e-143
BAG88167.1	Nod factor receptor protein [Glycine soja]	512	513	54%	4e-143
BAG88176.1	Nod factor receptor protein [Glycine max]	511	511	54%	8e-143
BAG88165.1	Nod factor receptor protein [Glycine soja]	511	511	54%	1e-142
BAG88160.1	Nod factor receptor protein [Glycine max]	511	511	54%	2e-142
BAG88154.1	Nod factor receptor protein [Glycine soja]	509	509	54%	4e-142
BAG88169.1	Nod factor receptor protein [Glycine max]	507	507	54%	2e-141
BAG88166.1	Nod factor receptor protein [Glycine max]	501	501	54%	9e-140
CAO22838.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	482	482	58%	8e-134
CAO22840.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	485	485	56%	7e-129
CAO22842.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	482	482	56%	4e-128
CAO22860.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	480	488	55%	9e-127
AAH819130.3	Putative protein kinase [Oryza sativa Japonica Group] >gb ABF94915.1 Protein kinase domain containing protein [Oryza sativa Japonica cultivar-group] >gb EAAZ28175.1 hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]	426	426	93%	5e-117
XP_004289236.1	hypothetical protein SORB1DRAFT_01g042230 [Sorghum bicolor] >gb EER95234.1 hypothetical protein SORB1DRAFT_01g042230 [Sorghum bicolor]	428	428	90%	5e-117 IG
EAY88155.1	hypothetical protein OsI_10648 [Oryza sativa Indica Group]	424	424	93%	2e-116
CAO22843.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	417	417	52%	3e-114
CAO22844.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	418	414	52%	1e-113
CAO22845.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	408	408	51%	1e-111
CAO22848.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	404	404	51%	2e-110
CAO22852.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	406	400	51%	3e-109
XP_004289238.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF45192.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	368	366	89%	6e-98 G
XP_002280793.1	PREDICTED: hypothetical protein [Vitis vinifera]	343	348	89%	1e-93 IG
CB228390.3	unnamed protein product [Vitis vinifera]	343	343	89%	3e-92
AA760791.1	SYM10-like protein [Galega orientalis]	336	336	40%	4e-90
ABR817033.1	unknown [Picea sitchensis]	333	333	77%	3e-89
CAH95762.1	hypothetical protein [Vitis vinifera]	328	328	89%	1e-87
XP_001787624.1	predicted protein [Physcomitrella patens subsp. patens] >gb EDQ67338.1 predicted protein [Physcomitrella patens subsp. patens]	309	309	91%	8e-82 IG
XP_002315653.1	predicted protein [Populus trichocarpa] >gb EEE89020.1 predicted protein [Populus trichocarpa]	308	308	76%	2e-81 IG
EAY07092.1	hypothetical protein OsI_08480 [Oryza sativa Indica Group]	299	299	88%	8e-79
CAO22850.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	298	298	40%	2e-78
BAL19270.1	LysM type receptor kinase [Lotus japonicus]	289	293	92%	5e-77
XP_001783689.1	predicted protein [Physcomitrella patens subsp. patens] >gb EDQ51621.1 predicted protein [Physcomitrella patens subsp. patens]	285	285	90%	1e-74 IG
XP_002328991.1	predicted protein [Populus trichocarpa] >gb EEE73851.1 predicted protein [Populus trichocarpa]	285	285	86%	1e-74 IG
XI_002316758.1	kinase, putative [Ricinus communis] >gb EEF52943.1 kinase, putative [Ricinus communis]	284	284	86%	2e-74 G
BAL19272.1	LysM type receptor kinase [Lotus japonicus] >dbj BA179287.1 LysM type receptor kinase [Lotus japonicus]	283	283	96%	5e-74
CB117583.3	unnamed protein product [Vitis vinifera]	277	277	93%	3e-72
XP_002328629.1	hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii] >gb EFJ08078.1 hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]	275	275	89%	2e-71 G
XP_002328644.1	hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii] >gb EFJ24716.1 hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]	273	273	89%	4e-71 IG
XP_002277331.1	PREDICTED: hypothetical protein [Vitis vinifera]	272	272	89%	8e-71 IG
XP_002289462.1	PREDICTED: hypothetical protein [Vitis vinifera]	268	268	93%	2e-69 G
BAL19276.1	LysM type receptor kinase [Lotus japonicus]	268	268	97%	2e-69
BAL19280.1	LysM type receptor kinase [Lotus japonicus]	267	267	97%	3e-69
XP_002329272.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29111.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	264	264	88%	3e-68 G
XP_002353278.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF29110.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	263	263	91%	4e-68 G
XP_002322982.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF38609.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	262	262	90%	1e-67 G
CSH46786.3	unnamed protein product [Vitis vinifera]	336	336	85%	9e-67

gE_002516233.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF52520.1	258	258	86%	2e-66	
XP_002269464.1	PREDICTED: hypothetical protein [Vitis vinifera]	258	258	86%	3e-66	
gE_002261889.1	PREDICTED: hypothetical protein [Vitis vinifera]	258	258	90%	2e-65	
XP_002310777.1	predicted protein [Populus trichocarpa] >gb EEF91227.1 predicted protein [Populus trichocarpa]	258	253	86%	6e-65	
ABG498515.1	LYK4 [Glycine max]	257	253	95%	8e-65	
gE_002321712.1	predicted protein [Populus trichocarpa] >gb EEF75190.1 predicted protein [Populus trichocarpa]	249	249	86%	3e-64	
NP_001949110.1	Osd6g0625200 [Oryza sativa Japonica Group] >dbj BAD35669.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAD37734.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAF20024.1 Osd6g0625200 [Oryza sativa Japonica Group] >dbj EAZ37689.1 hypothetical protein Os_J2029 [Oryza sativa Japonica Group]	242	242	86%	8e-62	
XP_002301898.1	predicted protein [Populus trichocarpa] >gb EEF94826.1 predicted protein [Populus trichocarpa]	239	239	86%	7e-61	
CAQ028863.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	238	238	21%	2e-60	
XP_002308949.1	ATP binding protein, putative [Ricinus communis] >gb EEF50927.1 ATP binding protein, putative [Ricinus communis]	238	238	91%	7e-60	
NP_06888362	CERK1 [CHITIN ELICITOR RECEPTOR KINASE 1]; kinase/ receptor signaling protein/ transmembrane + receptor protein kinase [Arabidopsis thaliana] >dbj BAF92785.1 chitin elicitor receptor kinase 1 [Arabidopsis thaliana]	229	229	81%	1e-57	
gE_002300083.1	predicted protein [Populus trichocarpa] >gb EEE84903.1 predicted protein [Populus trichocarpa]	224	224	91%	2e-56	
XP_002263870.1	PREDICTED: hypothetical protein [Vitis vinifera]	224	224	97%	3e-56	
C3H40964.3	unnamed protein product [Vitis vinifera]	224	224	97%	4e-56	

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

>gb ABQ59609.1 NFR5a [Glycine max]	
gb ADJ19105.1 Nod-factor receptor 5A [Glycine max]	
gb ADJ19108.1 Nod-factor receptor 5A [Glycine max]	
Length=598	
Score = 1058 bits (2737), Expect = 0.0, Method: Compositional matrix adjust.	
Identities = 527/598 (88%), Positives = 560/598 (93%), Gaps = 1/598 (0%)	
Query 1	MAVEFSLTLAGAILVYVIMFFTCICAGSQQTGNTNFCSPGNPSPSCETVYTYISQSEN 59
Sbjct 1	MAVEFSLTLAGAILVYVIMFFTCICAGSQQTGNTNFCSPGNPSPSCETVYTYISQSEN 60
Query 60	FLSLTTSVSNIFDTPSLIARASNLGHEEDKILPGCVLLIPVTCCTGNRSFANISYEINQ 119
Sbjct 61	FLSLTTSVSNIFDTPSLIARASNLGHEEDKILPGCVLLIPVTCCTGNRSFANISYEINQ 120
Query 120	GDSEFYVATTYQNLINWIAVMDLNPGLSQPTLPIGIVQVPLFCCKPSKNGLDKRGKYL 179
Sbjct 121	GDSEFYVATTYQNLINWIAVMDLNPGLSQPTLPIGIVQVPLFCCKPSKNGLDKRGKYL 180
Query 180	ITTVWQGNKVSFVSNKLGASPDQILSENNYQGNFTAAANLPVLIPVTLPLDILQSPDGG 239
Sbjct 181	ITTVWQGNKVSFVSNKLGASPDQILSENNYQGNFTAAANLPVLIPVTLPLDILQSPDGG 240
Query 240	RKRRIQLPVIIGTSLGCTLLVAVLAVLVVYVCLMRKINRSASSAETADKLLSGVSGVY 299
Sbjct 241	RKRRIQLPVIIGTSLGCTLLVAVLAVLVVYVCLMRKINRSASSAETADKLLSGVSGVY 300
Query 300	SKPTMYETDAIEMATNLSGCKIGSESVKANIEGKVLAVRKEDVTEELKILQKVNIG 359
Sbjct 301	SKPTMYETDAIEMATNLSGCKIGSESVKANIEGKVLAVRKEDVTEELKILQKVNIG 360
Query 360	NLVKLMGVSSDNGCNFVYVYEAENGSLDEWLFKSCSTSNRSASLTWCQRIISMAVDVY 419
Sbjct 361	NLVKLMGVSSDNGCNFVYVYEAENGSLDEWLFKSCSTSNRSASLTWCQRIISMAVDVY 420
Query 420	MGLYQYHEHAYPRIVRDTSSNILLSDNFKAIANTFMARTFTNPMKIDVFAFGVLL 479
Sbjct 421	MGLYQYHEHAYPRIVRDTSSNILLSDNFKAIANTFMARTFTNPMKIDVFAFGVLL 480
Query 480	IELLTGRKANTKENGSEVMILMKIDKIFQENREERLRKWMDEKLENYTYIDYALSIA 539
Sbjct 481	IELLTGRKANTKENGSEVMILMKIDKIFQENREERLRKWMDEKLENYTYIDYALSIA 540
Query 540	SLAVNCTADKSLSRPTIATVLSLTLTOPSPATILRSITSSGLDVEATQIVTSISAR 597
Sbjct 541	SLAVNCTADKSLSRPTIATVLSLTLTOPSPATILRSITSSGLDVEATQIVTSISAR 598

>gb ADJ19105.1 Nod-factor receptor 5A [Glycine max]	
Length=598	
GENE ID: 100498858 NFR5a [Nod-factor receptor 5A [Glycine max]]	
(10 or fewer PubMed links)	
Score = 1057 bits (2733), Expect = 0.0, Method: Compositional matrix adjust.	
Identities = 526/598 (87%), Positives = 560/598 (93%), Gaps = 1/598 (0%)	
Query 1	MAVEFSLTLAGAILVYVIMFFTCICAGSQQTGNTNFCSPGNPSPSCETVYTYISQSEN 59
Sbjct 1	MAVEFSLTLAGAILVYVIMFFTCICAGSQQTGNTNFCSPGNPSPSCETVYTYISQSEN 60

Query	60	FLSLTSTSVSNIFDTPSLTASRNQLQHEEDKLIPOGVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	61	FLSLT++SNIFDTPSLTASRNAL+ +DKLI QVLL+PVTGCTGNRSFANISYEINQ	120
Query	120	GDSEFPVATTLYQNLINHWAVMDNPLSGFTLPIGIVVPLFCCKPSKNGLDGIRKYL	179
Sbjct	121	GDSEFPVATT Y+NLITNW AVMDNP LS LPIGIVV PLFCCKPSKNGLD+ KYL	180
Query	180	ITVWQPCDNVSVFSNKLQASPDILSENNYQNTAASNLPVLIPVTLIPDLQSPSDG	239
Sbjct	181	ITVWQPCDNVSVLSDFGASPDIMSENNYQNTAANNLPVLIPVTLIPVLRSPSDG	240
Query	240	RKRIRGLPVIIGISGLCTLLVVSAILLVCCOLKMKSLNRSASSAEADKLLSGVSGVV	300
Sbjct	241	RKGRIRLPIVIGISGLCTLLVVLAVLVVYVYCKMKTINRSASSAEADKLLSGVSGVV	300
Query	300	SKPTMYETGATEATNLSLQCKIGESVYKANIEGKVLAVRKFEDVTEELKILQKVNIG	359
Sbjct	301	SKPTMYET A1+EAATNLSLQCKIGESVYKANIEGKVLAVRKFEDVTEELKILQKVNIG	360
Query	360	NLVKMGVSSDNDGNCFFVVEYAENGSL+EWLF+KSCB+TNSR SLTWQRIS+AVDV+	419
Sbjct	361	NLVKMGVSSDNDGNCFFVVEYAENGSLDWLFKSCBTSNRSASLTWQRISMAVDV+	420
Query	420	MCQYMHAEYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVVL	479
Sbjct	421	MCQYMHAEYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVVL	480
Query	480	TELTGRKAMTTKNGEVVLMKWDIKWIFDQENREERLKKWMDPKL+YYPIDVALSLA	539
Sbjct	481	TELTGRKAMTTKNGEVVLMKWDIKWIFDQENREERLKKWMDPKL+YYPIDVALSLA	540
Query	540	SLAVNCTADKLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSISAR	597
Sbjct	541	SLAVNCTADKLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSISAR	598

>gb|AD319107.1| **G** Nod-factor receptor 5A [Glycine max]
Length=598

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 1055 bits (2728), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/598 (87%), Positives = 560/598 (93%), Gaps = 1/598 (0%)

Query	1	MAVEFVSLTLAGLIQVLYVM+FTT-CICIAQSQQTNGNFCSPSPSPSCETVYVYISQSPN	59
Sbjct	1	MAVEF L L +QIL +VM F T I AQSQQ N TNFSCPS+SPSCETVYVY+QSPN	60
Query	60	FLSLTSTSVSNIFDTPSLTASRNQLQHEEDKLIPOGVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	61	FLSLT++SNIFDTPSLTASRNAL+ +DKLI QVLL+PVTGCTGNRSFANISYEINQ	120
Query	120	GDSEFPVATTLYQNLINHWAVMDNPLSGFTLPIGIVVPLFCCKPSKNGLDGIRKYL	179
Sbjct	121	GDSEFPVATT Y+NLITNW AVMDNP LS LPIGIVV PLFCCKPSKNGLD+ KYL	180
Query	180	ITVWQPCDNVSVFSNKLQASPDILSENNYQNTAASNLPVLIPVTLIPDLQSPSDG	239
Sbjct	181	ITVWQPCDNVSVLSDFGASPDIMSENNYQNTAANNLPVLIPVTLIPVLRSPSDG	240
Query	240	RKRIRGLPVIIGISGLCTLLVVSAILLVCCOLKMKSLNRSASSAEADKLLSGVSGVV	299
Sbjct	241	RKGRIRLPIVIGISGLCTLLVVLAVLVVYVYCKMKTINRSASSAEADKLLSGVSGVV	300
Query	300	SKPTMYETGATEATNLSLQCKIGESVYKANIEGKVLAVRKFEDVTEELKILQKVNIG	359
Sbjct	301	SKPTMYET A1+EAATNLSLQCKIGESVYKANIEGKVLAVRKFEDVTEELKILQKVNIG	360
Query	360	NLVKMGVSSDNDGNCFFVVEYAENGSL+EWLF+KSCB+TNSR SLTWQRIS+AVDV+	419
Sbjct	361	NLVKMGVSSDNDGNCFFVVEYAENGSLDWLFKSCBTSNRSASLTWQRISMAVDV+	420
Query	420	MCQYMHAEYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVVL	479
Sbjct	421	MCQYMHAEYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVVL	480
Query	480	TELTGRKAMTTKNGEVVLMKWDIKWIFDQENREERLKKWMDPKL+YYPIDVALSLA	539
Sbjct	481	TELTGRKAMTTKNGEVVLMKWDIKWIFDQENREERLKKWMDPKL+YYPIDVALSLA	540
Query	540	SLAVNCTADKLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSISAR	597
Sbjct	541	SLAVNCTADKLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSISAR	598

>gb|AD319112.1| **G** Nod-factor receptor 5B [Glycine max]
Length=599

GENE ID: 100498857 NFR5b | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score = 1029 bits (2661), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 330/599 (88%), Positives = 556/599 (92%), Gaps = 2/599 (0%)

Query	1	MAVEFVSLTLAGLIQVLYVM+FTT-CICIAQSQQTNGNFCSPSPSPSCETVYVYISQSPN	58
Sbjct	1	MAVEF L L +QIL +VM F T I AQSQQT N TNFSCPS+SPSCETVYVY+QSPN	60
Query	59	NFLSLTSTSVSNIFDTPSLTASRNQLQHEEDKLIPOGVLLIPVTCGCTGNRSFANISYEINQ	118
Sbjct	61	NFLSLT++SNIFDTPSLTASRNAL+ +DKLI QVLLIPVTCGCTGNRSFANISYEINQ	120
Query	119	GDSEFPVATTLYQNLINHWAVMDNPLSGFTLPIGIVVPLFCCKPSKNGLDGIRKYL	178
Sbjct	121	GDSEFPVATT Y+NLITNW AVMDNP LS LPIGIVV PLFCCKPSKNGLD+GIRKYL	180

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Sbjct 121 PQDSFPYVATTSYENLTNRVMDLNFSLSPNTLPIGIQVVFLECKCPKSNQLDGKIY 180
Query 179 LITHVQPKNDVNSVFNKLGASPDILSENNYGNFTAAANLVLVLPVTLFDLIQSPSD 238
LTHVQPKNDVNSVFNKLGASPDILSENNYGNFTAAANLVLVLPVTLFDLIQSPSD 240
Sbjct 181 LITHVQPKNDVNSVFNKLGASPDILSENNYGNFTAAANLVLVLPVTLFDLIQSPSD 240
Query 239 GRKHRIGLPVIIGISGLCTLLVVVSAITLVVCCVCKMKSINRASSAETADKLLGVSQY 298
RK I LPVIGISGLCTLLVVV A+LLV V CLK+KSIINRASSAETADKLLGVSQY 300
Sbjct 241 VARGGIRLPIVIGISGLCTLLVVVLAIVLVVYCYCLKIKSLINRASSAETADKLLGVSQY 300
Query 299 VSKPTMYETGAILEATMNLSEQCKIGESVYKIANIGKVLAVKRFKEDVTEELKILQKVNH 358
VSKPTMYETAI+EATMNLSEQCKIGESVYKIANIGKVLAVKRFK+VTEELKILQKVNH 360
Sbjct 301 VSKPTMYETDAINSEATMNLSEQCKIGESVYKIANIGKVLAVKRFK+VTEELKILQKVNH 360
Query 359 GNVLKMGVSSNDGNCFFVVEYA+NGSL+EWLF KSCS+TS+SR SLTWCRISIAIV 418
GNVLKMGVSSNDGNCFFVVEYA+NGSL+EWLF KSCS+TS+SR SLTWCRISIAIV 420
Sbjct 361 GNVLKMGVSSNDGNCFFVVEYA+NGSL+EWLF KSCS+TS+SR SLTWCRISIAIV 420
Query 419 SMGLQYMHSHAYPRIVHRTDTSNILLDSNFKRIANFSMARTFTNPMMSKIDVFAFGVV 478
+MGLQYMHSHAYPRIVHRTDTSNILLDSNFKRIANFSMARTFTNPMMSKIDVFAFGVV 480
Sbjct 421 SMGLQYMHSHAYPRIVHRTDTSNILLDSNFKRIANFSMARTFTNPMMSKIDVFAFGVV 480
Query 479 LIETLLGRKAMTTKENGVEVMLMKDWIKIFDQENNEERLAKWMDPRLQNYPIIDYALS 538
LIETLLGRKAMTTKENGVEVMLMKDWIKIFDQENNEERLAKWMDPRLQNYPIIDYALS 540
Sbjct 481 LIETLLGRKAMTTKENGVEVMLMKDWIKIFDQENNEERLAKWMDPRLQNYPIIDYALS 540
Query 539 ASLAVNCTADKSLRPTIAEIVLSISLITQPSPATIERSLTSGLDVEATQIVTSIAR 597
ASLAVNCTADKSLRPTIAEIVLSISLITQPSPATIERSLTSGLDVEATQIVTSIAR 599
Sbjct 541 ASLAVNCTADKSLRPTIAEIVLSISLITQPSPATIERSLTSGLDVEATQIVTSIAR 599

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>gb|ADJ19111.1| G Nod-factor receptor 5B [Glycine max]
Length=599

GENE ID: 100498857 NFR5b | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score = 1028 bits (2657), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 529/599 (88%), Positives = 555/599 (92%), Gaps = 2/599 (0%)

Query 1 MAVETVSLTAQAILLVVIM-FTTCIAAQSGQNTGTFNFCSPNSPSC-ETTVYVTSQSP 58
+AVETVSLTAQAILLVVIM-FTTCIAAQSGQNTGTFNFCSPNSPSC-ETTVYVTSQSP 60
Sbjct 1 MAVETVSLTAQAILLVVIM-FTTCIAAQSGQNTGTFNFCSPNSPSC-ETTVYVTSQSP 60
Query 59 NFSLTSISGNIFDTSPLSIARASNL+QHEEDKLIQGVLLIPVTCGCTGNRSFANISYEIN 118
NFSLTSISGNIFDTSPLSIARASNL+QHEEDKLIQGVLLIPVTCGCTGNRSFANISYEIN 120
Sbjct 61 NFSLTSISGNIFDTSPLSIARASNL+QHEEDKLIQGVLLIPVTCGCTGNRSFANISYEIN 120
Query 119 QDSFPYVATTYENLTNRVMDLNFSLSPNTLPIGIQVVFLECKCPKSNQLDGKIY 178
QDSFPYVATTYENLTNRVMDLNFSLSPNTLPIGIQVVFLECKCPKSNQLDGKIY 180
Sbjct 121 QDSFPYVATTYENLTNRVMDLNFSLSPNTLPIGIQVVFLECKCPKSNQLDGKIY 180
Query 179 LITHVQPKNDVNSVFNKLGASPDILSENNYGNFTAAANLVLVLPVTLFDLIQSPSD 238
LITHVQPKNDVNSVFNKLGASPDILSENNYGNFTAAANLVLVLPVTLFDLIQSPSD 240
Sbjct 181 LITHVQPKNDVNSVFNKLGASPDILSENNYGNFTAAANLVLVLPVTLFDLIQSPSD 240
Query 239 GRKHRIGLPVIIGISGLCTLLVVVSAITLVVCCVCKMKSINRASSAETADKLLGVSQY 298
RK I LPVIGISGLCTLLVVV A+LLV V CLK+KSIINRASSAETADKLLGVSQY 300
Sbjct 241 VARGGIRLPIVIGISGLCTLLVVVLAIVLVVYCYCLKIKSLINRASSAETADKLLGVSQY 300
Query 299 VSKPTMYETGAILEATMNLSEQCKIGESVYKIANIGKVLAVKRFKEDVTEELKILQKVNH 358
VSKPTMYETAI+EATMNLSEQCKIGESVYKIANIGKVLAVKRFK+VTEELKILQKVNH 360
Sbjct 301 VSKPTMYETDAINSEATMNLSEQCKIGESVYKIANIGKVLAVKRFK+VTEELKILQKVNH 360
Query 359 GNVLKMGVSSNDGNCFFVVEYA+NGSL+EWLF KSCS+TS+SR SLTWCRISIAIV 418
GNVLKMGVSSNDGNCFFVVEYA+NGSL+EWLF KSCS+TS+SR SLTWCRISIAIV 420
Sbjct 361 GNVLKMGVSSNDGNCFFVVEYA+NGSL+EWLF KSCS+TS+SR SLTWCRISIAIV 420
Query 419 SMGLQYMHSHAYPRIVHRTDTSNILLDSNFKRIANFSMARTFTNPMMSKIDVFAFGVV 478
+MGLQYMHSHAYPRIVHRTDTSNILLDSNFKRIANFSMARTFTNPMMSKIDVFAFGVV 480
Sbjct 421 SMGLQYMHSHAYPRIVHRTDTSNILLDSNFKRIANFSMARTFTNPMMSKIDVFAFGVV 480
Query 479 LIETLLGRKAMTTKENGVEVMLMKDWIKIFDQENNEERLAKWMDPRLQNYPIIDYALS 538
LIETLLGRKAMTTKENGVEVMLMKDWIKIFDQENNEERLAKWMDPRLQNYPIIDYALS 540
Sbjct 481 LIETLLGRKAMTTKENGVEVMLMKDWIKIFDQENNEERLAKWMDPRLQNYPIIDYALS 540
Query 539 ASLAVNCTADKSLRPTIAEIVLSISLITQPSPATIERSLTSGLDVEATQIVTSIAR 597
ASLAVNCTADKSLRPTIAEIVLSISLITQPSPATIERSLTSGLDVEATQIVTSIAR 599
Sbjct 541 ASLAVNCTADKSLRPTIAEIVLSISLITQPSPATIERSLTSGLDVEATQIVTSIAR 599

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>gb|ABQ59613.1| NFR5b [Glycine max]
Length=591

Score = 909 bits (2348), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 454/504 (90%), Positives = 474/504 (94%), Gaps = 0/504 (0%)

Query 94 QVLLIPVTCGCTGNRSFANISYEINQDSFPVATTYENLTNRVMDLNFSLSPNTLP 153
QVLLIPVTCGCTGNRSFANISYEINQDSFPVATTYENLTNRVMDLNFSLSPNTLP 154
Sbjct 12 QVLLIPVTCGCTGNRSFANISYEINQDSFPVATTYENLTNRVMDLNFSLSPNTLP 154
Query 154 IQIQVVFLECKCPKSNQLDGKIYLLITHVQPKNDVNSVFNKLGASPDILSENNYGN 213
IQIQVVFLECKCPKSNQLDGKIYLLITHVQPKNDVNSVFNKLGASPDILSENNYGN 214
Sbjct 72 IQIQVVFLECKCPKSNQLDGKIYLLITHVQPKNDVNSVFNKLGASPDILSENNYGN 214
Query 214 PTAAGNLVPLVPTLFDLIQSPSDGRKHRIGLPVIIGISGLCTLLVVVLAIVLVVYCY 193
PTAAGNLVPLVPTLFDLIQSPSDGRKHRIGLPVIIGISGLCTLLVVVLAIVLVVYCY 194
Sbjct 132 PTAAGNLVPLVPTLFDLIQSPSDGRKHRIGLPVIIGISGLCTLLVVVLAIVLVVYCY 194
Query 274 KMSINRASSAETADKLLGVSQYVSKPTMYETGAILEATMNLSEQCKIGESVYKIANE 333
+KSIINRASSAETADKLLGVSQYVSKPTMYETAI+EATMNLSEQCKIGESVYKIANE 334
Sbjct 192 KMSINRASSAETADKLLGVSQYVSKPTMYETGAILEATMNLSEQCKIGESVYKIANE 334
Query 334 GKVLAVKRFKEDVTEELKILQKVNHGNVLKMGVSSNDGNCFFVVEYA+NGSL+EWLF 393
GKVLAVKRFKEDVTEELKILQKVNHGNVLKMGVSSNDGNCFFVVEYA+NGSL+EWLF 394
Sbjct 252 GKVLAVKRFKEDVTEELKILQKVNHGNVLKMGVSSNDGNCFFVVEYA+NGSL+EWLF 394

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Query 394 KSCSETSGNRSTLTWCQRISIAVDVMSGLQYMHAYPRIVHRDITSSNILLDSNFKAKI 453
Sbjct 312 KSCSETSGNRSTLTWCQRISIAVDV+MGLQYMHAYPRIVHRDI SSNILLDSNFKAKI 371

Query 454 ANFSMARTFTNPMMSKIDVFAFGVVLIELLTGKRAMTTKENGVEVVMKADIKWIFDOEN 513
Sbjct 372 ANFSMARTFTND M KIDVFAFGVVLIELLTGKRAMTTKENGVEVVMKADIKWIFDOEN 431

Query 514 REERLKKWMDKLNLYPIDYALSLASIAVNCCTADKLSRSTIAEIVLSISLITQPSFAT 573
Sbjct 432 REERLKKWMDKLESTYPIDYALSLASIAVNCCTADKLSRSTIAEIVLSISLITQPSFAT 491

Query 574 LERSLTSSGLDVEATQIVTSISAR 597
Sbjct 492 LERSLTSSGLDVEATQIVTSIAAR 515

>emb|CA02593.1| SYM10 protein [Pisum sativum]
>emb|CA02594.1| SYM10 protein [Pisum sativum]
Length=594

Score = 870 bits (2247), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 437/600 (72%), Positives = 502/600 (83%), Gaps = 9/600 (1%)

Query 1 MAVFVSLTLGAQLIYVLMFF-TCIEAQSQQTNGTNFSCPNSSPPSCETVYVYISQSPN 59
Sbjct 1 MAVF L L + L+ LMFF T I AQ Q +GNFSCP +SPSCETVYVY +SPN 58
MAVF L +PSSSLIALMTLVVWISAGPLQSGTNFSCPSPSPSCETVYVYFASGN 58

Query 60 FILSTVSMNIFDTSPLSARASNLQHEEDKLLPGQVLLPVTCGCTGNRSFANISYEINQ 119
Sbjct 60 FILSTVSMNIFDTSPLSARASNL + + K L QVILPVTCGCTGNRSFANISYEINQ 118
FILSTNIGSIFDTSPLSARASNLDEEDKLLVEGQVLLPVTCGCTGNRSFANITYTIL 118

Query 120 GDSFVFATTIYQNLTNWAVMDLNPGLSQFTLPIGIQVVLPIECPKCPKSNGLDRGIKYL 179
Sbjct 119 GDSFVFATTIYQNLTNWAVMDLNPGLSQFTLPIGIQVVLPIECPKCPKSNGLDRGIKYL 178
GDSFVFATTIYQNLTNWAVMDLNPGLSQFTLPIGIQVVLPIECPKCPKSNGLDRGIKYL 178

Query 180 ITFVWQGNVNVSFVSNKLGASPDILSENNYQGNFTAASNLEVLPIVTLPLDLOSPDSG 239
Sbjct 180 ITFVWQGNVNVSFVSNKLGASPDILSENNYQGNFTAASNLEVLPIVTLPLDLOSPDSG 239
ITFVWQGNVNVSFVSNKLGASPDILSENNYQGNFTAASNLEVLPIVTLPLDLOSPDSG 239

Query 179 ITFVWQGNVNVSFVSNKLGASPDILSENNYQGNFTAASNLEVLPIVTLPLDLOSPDSG 236
Sbjct 179 ITFVWQGNVNVSFVSNKLGASPDILSENNYQGNFTAASNLEVLPIVTLPLDLOSPDSG 236
ITFVWQGNVNVSFVSNKLGASPDILSENNYQGNFTAASNLEVLPIVTLPLDLOSPDSG 236

Query 240 RWRHIGLPV-ITIGISGLCTLLVVSAILVVCVCLMKKSNRASSAETADKLLSGVSGY 296
Sbjct 240 RWRHIGLPV-ITIGISGLCTLLVVSAILVVCVCLMKKSNRASSAETADKLLSGVSGY 296
RWRHIGLPV-ITIGISGLCTLLVVSAILVVCVCLMKKSNRASSAETADKLLSGVSGY 296

Query 237 RKNSTQKPAFIIIGISGLCAFPVWTLISLVVYVCLMKKSNRASSAETADKLLSGVSGY 296
Sbjct 237 RKNSTQKPAFIIIGISGLCAFPVWTLISLVVYVCLMKKSNRASSAETADKLLSGVSGY 296
RKNSTQKPAFIIIGISGLCAFPVWTLISLVVYVCLMKKSNRASSAETADKLLSGVSGY 296

Query 299 VSKPTMYETGAILEATNLSLSEQCKIGSEVYKANIEGKVLAVKRFKEDVTEELIKLVQNNH 358
Sbjct 299 VSKPTMYETGAILEATNLSLSEQCKIGSEVYKANIEGKVLAVKRFKEDVTEELIKLVQNNH 358
VSKPTMYETGAILEATNLSLSEQCKIGSEVYKANIEGKVLAVKRFKEDVTEELIKLVQNNH 358

Query 359 GNVLKMGVSSDNDGNCFPVVEYAEAGSLDEWLFSE-SKTSNSVSLTWSGRTIAVAVD 418
Sbjct 359 GNVLKMGVSSDNDGNCFPVVEYAEAGSLDEWLFSE-SKTSNSVSLTWSGRTIAVAVD 418
GNVLKMGVSSDNDGNCFPVVEYAEAGSLDEWLFSE-SKTSNSVSLTWSGRTIAVAVD 418

Query 357 GNVLKMGVSSDNDGNCFPVVEYAEAGSLDEWLFSE-SKTSNSVSLTWSGRTIAVAVD 415
Sbjct 357 GNVLKMGVSSDNDGNCFPVVEYAEAGSLDEWLFSE-SKTSNSVSLTWSGRTIAVAVD 415
GNVLKMGVSSDNDGNCFPVVEYAEAGSLDEWLFSE-SKTSNSVSLTWSGRTIAVAVD 415

Query 419 SMGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGV 478
Sbjct 419 SMGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGV 478
SMGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGV 478

Query 479 LIELTGRKAMTTKENGVEVVMKADIKWIFDOENREERLKKWMDKLNLYPIDYALSL 538
Sbjct 479 LIELTGRKAMTTKENGVEVVMKADIKWIFDOENREERLKKWMDKLNLYPIDYALSL 538
LIELTGRKAMTTKENGVEVVMKADIKWIFDOENREERLKKWMDKLNLYPIDYALSL 538

Query 476 LIELTGRKAMTTKENGVEVVMKADIKWIFDOENREERLKKWMDKLNLYPIDYALSL 535
Sbjct 476 LIELTGRKAMTTKENGVEVVMKADIKWIFDOENREERLKKWMDKLNLYPIDYALSL 535
LIELTGRKAMTTKENGVEVVMKADIKWIFDOENREERLKKWMDKLNLYPIDYALSL 535

Query 539 ASIAVNCCTADKLSRSTIAEIVLSISLITQPSFAT-FLERSLTSSGLDVEATQIVTSISAR 597
Sbjct 536 ASIAVNCCTADKLSRSTIAEIVLSISLITQPSFAT-FLERSLTSSGLDVEATQIVTSISAR 597
ASIAVNCCTADKLSRSTIAEIVLSISLITQPSFAT-FLERSLTSSGLDVEATQIVTSISAR 597

>gb|ABJ19110.1| G truncated Nod-factor receptor 5A [Glycine max]
Length=501

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 866 bits (2238), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 434/501 (86%), Positives = 463/501 (92%), Gaps = 1/501 (0%)

Query 1 MAVFVSLTLGAQLIYVLMFF-TCIEAQSQQTNGTNFSCPNSSPPSCETVYVYISQSPN 59
Sbjct 1 MAVF L L + L+ LMFF T I AQSQ Q TNFSCPNSSPPSCETVYVY +SPN 60
MAVF L L + L+ LMFF T I AQSQ Q TNFSCPNSSPPSCETVYVY +SPN 60

Query 60 FILSTVSMNIFDTSPLSARASNLQHEEDKLLPGQVLLPVTCGCTGNRSFANISYEINQ 119
Sbjct 60 FILSTVSMNIFDTSPLSARASNLQHEEDKLLPGQVLLPVTCGCTGNRSFANISYEINQ 119
FILSTVSMNIFDTSPLSARASNLQHEEDKLLPGQVLLPVTCGCTGNRSFANISYEINQ 119

Query 120 GDSFVFATTIYQNLTNWAVMDLNPGLSQFTLPIGIQVVLPIECPKCPKSNGLDRGIKYL 179
Sbjct 120 GDSFVFATTIYQNLTNWAVMDLNPGLSQFTLPIGIQVVLPIECPKCPKSNGLDRGIKYL 179
GDSFVFATTIYQNLTNWAVMDLNPGLSQFTLPIGIQVVLPIECPKCPKSNGLDRGIKYL 179

Query 180 ITFVWQGNVNVSFVSNKLGASPDILSENNYQGNFTAASNLEVLPIVTLPLDLOSPDSG 239
Sbjct 180 ITFVWQGNVNVSFVSNKLGASPDILSENNYQGNFTAASNLEVLPIVTLPLDLOSPDSG 239
ITFVWQGNVNVSFVSNKLGASPDILSENNYQGNFTAASNLEVLPIVTLPLDLOSPDSG 239

Query 240 RWRHIGLPV-ITIGISGLCTLLVVSAILVVCVCLMKKSNRASSAETADKLLSGVSGY 299
Sbjct 240 RWRHIGLPV-ITIGISGLCTLLVVSAILVVCVCLMKKSNRASSAETADKLLSGVSGY 299
RWRHIGLPV-ITIGISGLCTLLVVSAILVVCVCLMKKSNRASSAETADKLLSGVSGY 299

Query 300 SKPTMYETGAILEATNLSLSEQCKIGSEVYKANIEGKVLAVKRFKEDVTEELIKLVQNNH 359
Sbjct 300 SKPTMYETGAILEATNLSLSEQCKIGSEVYKANIEGKVLAVKRFKEDVTEELIKLVQNNH 359
SKPTMYETGAILEATNLSLSEQCKIGSEVYKANIEGKVLAVKRFKEDVTEELIKLVQNNH 359

Query 360 GNVLKMGVSSDNDGNCFPVVEYAEAGSLDEWLFSE-SKTSNSVSLTWSGRTIAVAVD 419
Sbjct 361 GNVLKMGVSSDNDGNCFPVVEYAEAGSLDEWLFSE-SKTSNSVSLTWSGRTIAVAVD 419
GNVLKMGVSSDNDGNCFPVVEYAEAGSLDEWLFSE-SKTSNSVSLTWSGRTIAVAVD 419

Query 420 MGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGV 479
Sbjct 421 MGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGV 480
MGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGV 480

Query 480 IELLTGRKAMTTKENGVEVVM 500

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Sbjct 481 IELLTGRKAMTTKNGEVVLM
IELLTGRKAMTTKNGEVVLM 501

>emb|CAK02595.1| SYM10 protein [Pisum sativum]
emb|CAK02596.1| SYM10 protein [Pisum sativum]
gb|AB045277.1| Nod factor recognition protein [Pisum sativum]
Length=594

Score = 865 bits (2236), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 435/600 (72%), Positives = 501/600 (83%), Gaps = 9/600 (1%)

Query 1 MAVFEVSLTGAQILVYVMEFT-TCIEAQSQQTNGTNFSCPSNPSPSCETVYVYISQSN 59
Sbjct 1 MAVFE L + L++ IMFT T I AQ Q +GTNFCPC +SPSCETVYVY +SFN 58
MAIFF--LPSSSRHLLALMTFTVFNISQAQLGLSGTNFCPCFDSFSPSCETVYVYFAKSN

Query 60 FLSTLSVSNIFDTPSLTARASNLQHEEDKLPGQVLLIPVTCGCTGNRSFANISYEINQ 119
Sbjct 59 FLSTNLQSIDFDTPSLTAKASNIQHEEDKLQVGVLLIPVTCGCTNRNRYFANFTYIKL 118

Query 120 GDSYFVATTIYNLTNHWAMVLDNPLSGQFTLPIGIVVPLFCCKPSKNGLDGKIKYL 179
Sbjct 119 GUNYFVTSYQNTLTNYEMENFNPLSPNLLPEIKVYVPLFCCKPSKNGLSKGIKHL 178

Query 180 ITHVWQNDNVSVFVSKLGASQDILBENNYQNFTAAASNLVPLIPVTLPLDQSPSDG 239
Sbjct 179 ITHVWQNDNV SVK GAS D +ENN QNFTA+N+P+LIPVT LP+ Q S+G 236
ITVYWKANDVSVSKAGVAVMGTEMN--QNFASVNTPLIPVTLPLDQPSMG

Query 240 RKRHRTGLV-IIGISGLCTLLVVSAILLVVCCLMKRSNRSASSAETADKLLSGVSGY 298
Sbjct 237 RKRNTKPFPIIGISGLGAPVVLITSLVYVYCLMKRLNRSTSAETADKLLSGVSGY 296

Query 299 VSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGVAVLRKFEDEVTEELIKLQKVNH 358
Sbjct 297 VSKPTMYEDIMEATMNLSENCKIGESVYKANIDGRVAVLRKIKDADEALIKLQKVNH 356

Query 359 GNVLKMGVSDNDGNCFFVVEYAENGSLSEWLEPAKSCSETSNRSRTSLTWCRISIAVDV 418
Sbjct 357 GNVLKMGVSDNDGNCFLVVEYAENGSLSEWLEFS--LSKTSNSVSLTWGRTIAVDV 415

Query 419 SMGLQYMHSHAYPRIVHRTDTSNILLDSNFKAIANFSMARTTNPMMKIDVFAFGVV 478
Sbjct 416 AVGLQYMHSHAYPRIVHRTDTSNILLDSNFKAIANFSMARTTNSNMMKIDVFAFGVV 475

Query 479 LLELTGRKAMTTKNGEVVLMKMDIKWIFDQENREERLRKMDPKLDNYYPIDYALS 538
Sbjct 476 LLELTGRKAMTT KNGEVVLMKMDIKWIFDQENREERLRKMDPKLDNYYPIDYALS 535

Query 539 ASLAVNCTADKLSRPTIAEIVLSLSLTQPSA-FLERSLTSSGLDVEATQIVTSISAR 597
Sbjct 536 ASLAVNCTADKLSRPTIAEIVLSLSLTQPSA-FLERSLTSSGLDVEATQIVTSISAR 594

>emb|CAK02597.1| G Nod-factor receptor 5 [Lotus japonicus]
emb|CAK02598.1| G Nod-factor receptor 5 [Lotus japonicus]
Length=595

GENE ID: 100034751 NFR5 | Nod-factor receptor 5 [Lotus japonicus]
(10 or fewer PubMed links)

Score = 862 bits (2277), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 432/601 (71%), Positives = 502/601 (83%), Gaps = 10/601 (1%)

Query 1 MAVFEVSLTGAQILVYVMEFT-TEAQSQQTNGTNFSCPSNPSPSCETVYVYISQSN 59
Sbjct 1 MAVFE LT G+ L++ L I A+S++ +G +FSCP +SPSCETVYVY +QSFN 58
MAVFE--LTSGSLSLFLALTLFTNTAARSEKISGDFSCFDSFSPSCETVYVYTAQSN

Query 60 FLSTLSVSNIFDTPSLTARASNLQHEEDKLPGQVLLIPVTCGCTGNRSFANISYEINQ 119
Sbjct 59 FLST++S+IFD SPISLARAS++ +KRLPGQVLLIPVTCGCG GN S AN SY+I 118
LSTNLQSIDFDTPSLTAKASNIQAGKLVGVLLIPVTCGCGGNSASNTYQIOL

Query 120 GDSYFVATTIYNLTNHWAMVLDNPLSGQFTLPIGIVVPLFCCKPSKNGLDGKIKYL 179
Sbjct 119 GDSYDFVATTIYNLTNWNVQASNPGVNPLYLPERVKVYVPLFCRCPSPKNGLKGQYVL 178

Query 180 ITHVWQNDNVSVFVSKLGASQDILBENNYQNFTAAASNLVPLIPVTLPLDQSPSDG 239
Sbjct 179 ITHVWQNDNVSVS K GASD IL+EN YGQ+FTAA+NL+LIPVT LP+L Q S+G 236
ITVYWKANDVSVLSAKGASPADILFENRYGQFTAAATNLPLIFVTLPLDQPSMG

Query 240 RKRHRTGLV-IIGISGLCTLLVVSAILLVVCCLMKRSNRSASSAETADKLLSGVSGY 298
Sbjct 239 RKRSLITLIGITLIGTLLTAVLTGTLVYVYCRKKAIRNTASSAETADKLLSGVSGY 296

Query 299 SKPTMYETGAILEATMNLSEQCKIGESVYKANIEGVAVLRKFE-DVTEELIKLQKVNH 358
Sbjct 297 SKPNVYEIDIMEATKQPSDECKVGEVYKANIEGRVAVLRKIKGEGANEEIKLQKVNH 356

Query 359 GNVLKMGVSDNDGNCFFVVEYAENGSLSEWLEPAKSCSETSNRSRTSLTWCRISIAVDV 418
Sbjct 357 GNVLKMGVSDNDGNCFLVVEYAENGSLSEWLEFS--LSKTSNSVSLTWGRTIAVDV 415

Query 419 SMGLQYMHSHAYPRIVHRTDTSNILLDSNFKAIANFSMARTTNPMMKIDVFAFGVV 478
Sbjct 416 AVGLQYMHSHAYPRIVHRTDTSNILLDSNFKAIANFSMARTTNSNMMKIDVFAFGVV 475

Query 479 LLELTGRKAMTTKNGEVVLMKMDIKWIFDQENREERLRKMDPKLDNYYPIDYALS 538
Sbjct 476 LLELTGRKAMTTKNGEVVLMKMDIKWIFDQENREERLRKMDPKLDNYYPIDYALS 535

Query 539 ASLAVNCTADKLSRPTIAEIVLSLSLTQPSA-FLERSLTSSGLDVEATQIVTSISAR 596
Sbjct 535 ASLAVNCTADKLSRPTIAEIVLSLSLTQPSA-FLERSLTSSGLDVEATQIVTSISAR 594

Query 597 R 597
Sbjct 595 R 595

gfp ABF50224.1		No factor perception protein (Medicago truncatula)	
length=595			
Score = 839 bits (2169),		Expect = 0.0, Method: Compositional matrix adjust.	
Identities = 422/599 (70.4%),		Positives = 493/599 (82%), Gaps = 6/599 (1%)	
Query	1	MAVFFSLTGLAQIQLVLMFFFLCIRGASQQTNTNFCSPNSPSPCEYTVYVYQSINF	60
Sbjct	1	MSAFFPSSHSLGLVLMFLPFLNLSLQIYLSISTMTQVDSVPSCETVYVYQAQINF	60
Query	61	LSITSTSTPTDPSIRLALQSLHDEKIPGLQVLLPVTCQGRNFANISYIMQCS	120
Sbjct	61	LSISLSTPTDPSIRLALQSLHDEKIPGLQVLLPVTCQGRNFANISYIMQCS	120
Query	121	DSYFVYATVITNIMHADVMDLPGISQTLPGIIVLVFLCCKNSFANITYSIKRG	180
Sbjct	121	DNFISITSTPTDPSIRLALQSLHDEKIPGLQVLLPVTCQGRNFANISYIMQCS	180
Query	181	THVQNDVYFVBNKIGASPDIISENYYGNTATSNLVLPIVTLPLDQISFGR	240
Sbjct	181	THVQNDVYFVBNKIGASPDIISENYYGNTATSNLVLPIVTLPLDQISFGR	240
Query	241	KHRTGLVITISQTLTLLVVSALIVCVCLRMKINSRGSAAFLAKLPGSVY	300
Sbjct	241	KHRTGLVITISQTLTLLVVSALIVCVCLRMKINSRGSAAFLAKLPGSVY	300
Query	300	KPTMYETGATLNLMLSEQKISGVYKANIGKVLAVKPKKDETEELIKLQVNH	360
Sbjct	300	KPTMYETGATLNLMLSEQKISGVYKANIGKVLAVKPKKDETEELIKLQVNH	360
Query	360	NVLKLVYSSNDGNCVFVEYASNGSLVFLAKSCSTNTSRSTVWQRIADV	420
Sbjct	360	NVLKLVYSSNDGNCVFVEYASNGSLVFLAKSCSTNTSRSTVWQRIADV	420
Query	420	GLQVMEHYPRVIRHRTISNLLSFKATKAKANSMAARTNPMMSKILQVAFGV	480
Sbjct	420	GLQVMEHYPRVIRHRTISNLLSFKATKAKANSMAARTNPMMSKILQVAFGV	480
Query	480	TELTGRAMTTKEGTVIWMKIDKIFPDQEEENRELRKMDKESYINPIDALSA	540
Sbjct	480	TELTGRAMTTKEGTVIWMKIDKIFPDQEEENRELRKMDKESYINPIDALSA	540
Query	540	SLAVNCTADKRSKPTIAEIVLSLISLQSPMLASLTLRSLTSGSLQVATQVTSIR	600
Sbjct	540	SLAVNCTADKRSKPTIAEIVLSLISLQSPMLASLTLRSLTSGSLQVATQVTSIR	600
Query	595	SLAVNCTADKRSKPTIAEIVLSLISLQSPMLASLTLRSLTSGSLQVATQVTSIR	595

amb CA002956.1	Ly- domain containing receptor-like kinase [Medicago truncatula, vnr. truncatula]	
Length=498		
Score = 740 bits (1910), Expect = 0.0, Method: Compositional matrix adjust.		
Identities = 358/497 (72%), Positives = 420/497 (84%), Gaps = 4/497 (0%)		
Query 45	PGCETVYVYVGGSTNLSLVSINFDTSPLTSIPASRANSLGHEDEKLLPGVLLVLPVFTGC	104
Sbjct 4	PGCETVYVYVGGSTNLSLVSINFDTSPLTSIPASRANSLGHEDEKLLPGVLLVLPVFTGC	104
Query 105	TGNSFANSISVEINQGSDFYVATTLVYNLTWIAWMDINPGLSGLTLPGLIVQVPLFC	124
Sbjct 4	TGNSFANSISVEINQGSDFYVATTLVYNLTWIAWMDINPGLSGLTLPGLIVQVPLFC	124
Query 165	KCPKSNLQDRIQLYLTTHWQDINVSFVNLKSGAPDILLENNGVPTFASNLVPL	224
Sbjct 124	KCPKSNLQDRIQLYLTTHWQDINVSFVNLKSGAPDILLENNGVPTFASNLVPL	224
Query 125	FVTLDELQDSFSDGKRRKI--GLVPIGLISGCTGLTVLISLVLCVCCAKMSNSNAS	283
Sbjct 182	FVTLDELQDSFSDGKRRKI--GLVPIGLISGCTGLTVLISLVLCVCCAKMSNSNAS	283
Query 284	SAETADKLISGVSGYKPTMYEATL+TWNLS+CRIGESVYVANN+GLVAF+K	341
Sbjct 242	SAETADKLISGVSGYKPTMYEATL+TWNLS+CRIGESVYVANN+GLVAF+K	341
Query 344	EDVTEKLLQKVNHNVLKVMGSSDNCNCP+VYVEAENGSLWFLPACSSTENSR	403
Sbjct 302	EDVTEKLLQKVNHNVLKVMGSSDNCNCP+VYVEAENGSLWFLPACSSTENSR	403
Query 404	TSLVQGRISAVDVMISGLQVSHAYPAIVRHVITSSNILLDSNFKAKIANFMSARTT	463
Sbjct 361	TSLVQGRISAVDVMISGLQVSHAYPAIVRHVITSSNILLDSNFKAKIANFMSARTT	463
Query 464	NPMISKIDVFAFVGLIETLTKGAKMTTKEGSEVIMLMKDQWIFPDQEEANRERLRKD	523
Sbjct 524	NPMISKIDVFAFVGLIETLTKGAKMTTKEGSEVIMLMKDQWIFPDQEEANRERLRKD	523
Query 481	PKLQNYDIDVDAISLAS 540	
Sbjct 481	PKLQNYDIDVDAISLAS 497	

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>embL|CA02958.1| Ly-domain containing receptor-like ligand [Medicago truncatula
var. truncatula]
length=32
Score = 733 bits (189%), Expect = 0.0, Method: Compositional matrix adjust.
Identifiers = 355/494 (71%), Positives = 417/494 (84%), gap = 4/94 (0%)

Query 48 ETVYTVYVQSPNPLSLIISITSVNIPEDTSPSLIAANLQWEEDIKLQPVLLIVPTGCTGN
ETVTVYVQSPNPLSLIISITSVNIPEDTSPSLIAANLQWEEDIKLQPVLLIVPTGCTGN 107
Sbjct 1 ETVYTVYVQSPNPLSLIISITSVNIPEDTSPSLIAANLQWEEDIKLQPVLLIVPTGCTGN
60

Query 108 RSPANSTVYVQSPNPLSLIISITSVNIPEDTSPSLIAANLQWEEDIKLQPVLLIVPTGCTGN
RSPANSTVYVQSPNPLSLIISITSVNIPEDTSPSLIAANLQWEEDIKLQPVLLIVPTGCTGN 167
Sbjct 61 RSPANSTVYVQSPNPLSLIISITSVNIPEDTSPSLIAANLQWEEDIKLQPVLLIVPTGCTGN
120

Query 168 SKNOLDGRGKLVITHWQNPVSNVSKNGLSPDILSENNYQGNFAASNPLVPT
SKNOLDGRGKLVITHWQNPVSNVSKNGLSPDILSENNYQGNFAASNPLVPT 227

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Sbjct 121 SKNQI++GIKYLIT+VMQ NDNV+ VS+K GAS ++L+ENN+ NFTA++M VLIPT 178
 SKNQI+NGIKYLYITVVMQNDNVITVSSKPGASQVEMLAENN--NFTASTNRSLVITPT
 Query 228 LPLDQISPSDGRKHRI-GLPVIIGISGLCTLLVVVAAILVVCCLMKMLNRSASAE 286
 LP L Q +8GRK L +IIGISGL +V + IV V CLMK LNRS SS+E
 Sbjct 179 SLPLQDQPSNGRKRSSQNIALIIGISGLSAFFLIVITLSLVVYVCLMKMLNRSSTSE 238
 SLPLQDQPSNGRKRSSQNIALIIGISGLSAFFLIVITLSLVVYVCLMKMLNRSSTSE
 Query 287 TADKLISGVSGVSKPTMYTGALILEATMNLSEQCKIGESVYKANI+GKVLAVKRFKEDV 346
 TADKLISGVSGVSKPTMYTGALILEATMNLSEQCKIGESVYKANI+GKVLAVKRFKEDV
 Sbjct 239 TADKLISGVSGVSKPTMYTGALILEATMNLSEQCKIGESVYKANI+GKVLAVKRFKEDV 298
 TADKLISGVSGVSKPTMYTGALILEATMNLSEQCKIGESVYKANI+GKVLAVKRFKEDV
 Query 347 TELKILQKVNHNKLMVSSDNDGNCPLVYEAENGSLSEMLF+S S+TNS SL 406
 +TELKILQKVNHNKLMVSSDNDGNCPLVYEAENGSLSEMLF+S S+TNS SL
 Sbjct 299 SEELKILQKVNHNKLMVSSDNDGNCPLVYEAENGSLSEMLF+S S+TNS SVSL 357
 SEELKILQKVNHNKLMVSSDNDGNCPLVYEAENGSLSEMLF+S S+TNS SVSL
 Query 407 TWQRCISAVDSMGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNM 466
 TW QR +IA+DV++GLQVMEH YPRIVHRDIT+SNILL SNFKAKIANF MART TN M
 Sbjct 358 TWQRCIATMVAIGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNM 417
 TWQRCIATMVAIGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNM
 Query 467 MKFI DVAFGVLLITLTKRKAMTTKENGVEVVLMDKFIQDOENREERLRKMMDPKL 526
 M K I DVAFGVLLITLTKRKAMTTKENGVEVVLMDKFIQDOENREERLRKMMDPKL
 Sbjct 418 MKFI DVAFGVLLITLTKRKAMTTKENGVEVVLMDKFIQDOENREERLRKMMDPKL 477
 MKFI DVAFGVLLITLTKRKAMTTKENGVEVVLMDKFIQDOENREERLRKMMDPKL
 Query 527 DWYYPIDYALSLAS 540
 ++YPID ALS+AS
 Sbjct 478 ESFYPIDNALSMAS 491
 ESFYPIDNALSMAS
 >emb|CA002933.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002934.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002935.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 10 more sequence titles
 emb|CA002938.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002939.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002940.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002941.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002942.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002943.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002944.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002945.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002946.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002947.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002948.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002949.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002950.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002951.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002952.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002953.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002954.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002955.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002956.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002957.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002958.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002959.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002960.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002961.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002962.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002963.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002964.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002965.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002966.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002967.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002968.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002969.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002970.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002971.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002972.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002973.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CA002974.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=487
 Score = 725 bits (1871), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 351/489 (71%), Positives = 413/489 (84%), Gaps = 4/489 (0%)
 Query 53 YIQSPNPLSISLTVSNIFDTPSLSTARASNLQHEEDKLIPOGVLLIPVTCOCTGNRSFAN 112
 Y +QSPNPLSL++S+IP+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCOCT GN SFAN
 Sbjct 1 YRAQSPNPLSISLNTSIDFNLSPRLAKASNIEADKLIPOQLLVLPVTCOCTGNHSFAN 60
 YRAQSPNPLSISLNTSIDFNLSPRLAKASNIEADKLIPOQLLVLPVTCOCTGNHSFAN
 Query 113 ISYEINGDSIFYPVATLITQNLNHWAVMLNPLGSQFTLPDITGVQVPLFCCKPSKNQJL 172
 +Y I GDS+P+ ++ T QNLNHW + NP LS LP+ +Y +PLFCCKPSKNQJL
 Sbjct 61 ITYSIKGDSNFIPLSITSYQNLNHWAVMLNPLGSQFTLPDITGVQVPLFCCKPSKNQJL 120
 ITYSIKGDSNFIPLSITSYQNLNHWAVMLNPLGSQFTLPDITGVQVPLFCCKPSKNQJL
 Query 173 DRGKYLIT+VMQ NDNV+ VS+K GAS ++L+ENN+ NFTA++M VLIPT LP L 232
 +GIKYLIT+VMQ NDNV+ VS+K GAS ++L+ENN+ NFTA++M VLIPT LP L
 Sbjct 121 NKGIKYLIT+VMQ NDNVITVSSKPGASQVEMLAENN--NFTASTNRSLVITPTSLPLK 178
 NKGIKYLIT+VMQ NDNVITVSSKPGASQVEMLAENN--NFTASTNRSLVITPTSLPLK
 Query 233 IQSPSDGRKHRI-GLPVIIGISGLCTLLVVVAAILVVCCLMKMLNRSASAEADKL 291
 Q +8GRK L +IIGISGL +V + IV V CLMK LNRS SS+ETADKL
 Sbjct 179 IQSPSDGRKRSSQNIALIIGISGLSAFFLIVITLSLVVYVCLMKMLNRSSTSEADKL 238
 IQSPSDGRKRSSQNIALIIGISGLSAFFLIVITLSLVVYVCLMKMLNRSSTSEADKL
 Query 292 LSGVSGVSGVSKPTMYTGALILEATMNLSEQCKIGESVYKANI+GKVLAVKRFKEDVTELK 351
 LSGVSGVSGVSKPTMYTGALILEATMNLSEQCKIGESVYKANI+GKVLAVKRFKEDVTELK
 Sbjct 239 LSGVSGVSGVSKPTMYTGALILEATMNLSEQCKIGESVYKANI+GKVLAVKRFKEDVTELK 298
 LSGVSGVSGVSKPTMYTGALILEATMNLSEQCKIGESVYKANI+GKVLAVKRFKEDVTELK
 Query 352 ILQKVNHNKLMVSSDNDGNCPLVYEAENGSLSEMLF+S S+TNS SLTW OR 411
 ILQKVNHNKLMVSSDNDGNCPLVYEAENGSLSEMLF+S S+TNS SLTW OR
 Sbjct 299 SEELKILQKVNHNKLMVSSDNDGNCPLVYEAENGSLSEMLF+S S+TNS SVSLTW 357
 SEELKILQKVNHNKLMVSSDNDGNCPLVYEAENGSLSEMLF+S S+TNS SVSLTW
 Query 412 ISIAVDVSMGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNMMDK 471
 +IA +DV++GLQVMEH YPRIVHRDIT+SNILL SNFKAKIANF MART TN NM KD
 Sbjct 358 ITIATMVAIGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNMMDK 417
 ITIATMVAIGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNMMDK
 Query 472 VFAPGVLLITLTKRKAMTTKENGVEVVLMDKFIQDOENREERLRKMMDPKLWYYP 531
 VFAPGVLLITLTKRKAMTTKENGVEVVLMDKFIQDOENREERLRKMMDPKLWYYP
 Sbjct 418 VFAPGVLLITLTKRKAMTTKENGVEVVLMDKFIQDOENREERLRKMMDPKLWYYP 477
 VFAPGVLLITLTKRKAMTTKENGVEVVLMDKFIQDOENREERLRKMMDPKLWYYP
 Query 532 IDVALSLAS 540
 ID ALS+AS
 Sbjct 478 IDNALSMAS 496
 IDNALSMAS
 >emb|CA002940.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=487
 Score = 723 bits (1866), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 351/489 (71%), Positives = 412/489 (84%), Gaps = 4/489 (0%)
 Query 53 YIQSPNPLSISLTVSNIFDTPSLSTARASNLQHEEDKLIPOGVLLIPVTCOCTGNRSFAN 112
 Y +QSPNPLSL++S+IP+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCOCT GN SFAN
 Sbjct 1 YRAQSPNPLSISLNTSIDFNLSPRLAKASNIEADKLIPOQLLVLPVTCOCTGNHSFAN 60
 YRAQSPNPLSISLNTSIDFNLSPRLAKASNIEADKLIPOQLLVLPVTCOCTGNHSFAN

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Query 113 TSVEINQGSDFYFVATTLYQNLTNWHAVMDINPGLSQPTLPDPIGQVVIPLFCCKPSKNQL 172
Sbjct 61 I+Y I GSD+P+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCCKPSKNQL 120
TSYIKQGNFTLSITSYQNLTNLYLFKNFNNPNSPTLLPLDTKVSVPFLFCCKPSKNQL

Query 173 DRGKYLITHVQNDVNSVFNKLGASQDILSENNGQNTAASNLPVLPVTLPLDL 232
+GIGYLIIT+VWQ DNV+ VS+K GAS ++L+ENN+ NPTA++N VLIPTV LP L
Sbjct 121 NKGIKYLITYVQNDNVTLVSSKFGASQVEMLAENN+-NFTASTNRSVLIPVTLPLK 178

Query 233 IQGSPSDGRKRI+GLPVIIGISLGCCTLLVVVSAILLVCCCLMKKSLNRSSAETAADKL 291
Q S+GRK L+IIGISIG ++V + IV V CLMK LNRS SS+ETADKL
Sbjct 179 DQPSNDRGRSSQNLALLIGISLGSAPFLLVLTLSLVVYVCLMKKSLNRSSAETAADKL 238

Query 292 LSGVSGYVSKFTMYETQALIAEMNLSEQCCKIGESVYKANIIGKVLAVKRFKEDYTEELK 351
LSGVSGYVSKFTMYE AI+E T NLS+ CKIGESVYKANI+G+VLAVK+ R+D +EELK
Sbjct 239 LSGVSGYVSKFTMYEIDAMEGTNLSDNCKIGESVYKANIDGRVLAVKKIKKASEELK 296

Query 352 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLSEELFAKSCSETSNRSRTLTWCOR 411
ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLSEELF++S +TSNS SLTW GR
Sbjct 299 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLSEELFSEB-SKTSNSVSVLTSWGR 357

Query 412 ISIAVDVSMGLQYMERHAYPRIVHRDITSSNLLDSNFKAKIANFSGMARTFNNPMKKID 471
++IA+DV++GLQYMERH YPRI+HRDIT+SNLL SNFKAKIANF MART TN MM KID
Sbjct 358 ITIAMDVAIGLQYMERHYPRIIHRDITTSNLLDSNFKAKIANFGMARTSNMMPKID 417

Query 472 VFAFGVLLIELLTGKRAMTTKENGSEVVMKMDIKWIFDQENREERLRKMDPKLDNYP 531
VFAFGVLLIELLTG+KAMTTKENGSEV+LMD KRIID E NREERLRKMDPKL++Y+P
Sbjct 418 VFAFGVLLIELLTGKAMTTKENGSEVVLKMDKFWKIFDLEGNREERLRKMDPKLESFYP 477

Query 532 IDVALSIAS 540
ID ALSIAS
Sbjct 478 IDVALSIAS 486

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>emb|CA002951.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=487

Score = 723 bits (1866), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 351/489 (71%), Positives = 412/489 (84%), Gaps = 4/489 (0%)

```

Query 53 YIQSGPNFLSITSVSNIFDPSLSTARASNLQHEEDKLIPQVLLIPVTCCTGNRSGFAN 112
Sbjct 1 Y+QSGPNFLS++S+IP+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN 60
YRAQSGPNFLSISNIDITNPLSLPIAKASNIEADKRLPDQLLLVPVTCCTGNRSGFAN

Query 113 TSVEINQGSDFYFVATTLYQNLTNWHAVMDINPGLSQPTLPDPIGQVVIPLFCCKPSKNQL 172
+Y I GSD+P+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCCKPSKNQL
Sbjct 61 I+Y I GSD+P+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCCKPSKNQL 120
TSYIKQGNFTLSITSYQNLTNLYLFKNFNNPNSPTLLPLDTKVSVPFLFCCKPSKNQL

Query 173 DRGKYLITHVQNDVNSVFNKLGASQDILSENNGQNTAASNLPVLPVTLPLDL 232
+GIGYLIIT+VWQ DNV+ VS+K GAS ++L+ENN+ NPTA++N VLIPTV LP L
Sbjct 121 NKGIKYLITYVQNDNVTLVSSKFGASQVEMLAENN+-NFTASTNRSVLIPVTLPLK 178

Query 233 IQGSPSDGRKRI+GLPVIIGISLGCCTLLVVVSAILLVCCCLMKKSLNRSSAETAADKL 291
Q S+GRK L+IIGISIG ++V + IV V CLMK LNRS SS+ETADKL
Sbjct 179 DQPSNDRGRSSQNLALLIGISLGSAPFLLVLTLSLVVYVCLMKKSLNRSSAETAADKL 238

Query 292 LSGVSGYVSKFTMYETQALIAEMNLSEQCCKIGESVYKANIIGKVLAVKRFKEDYTEELK 351
LSGVSGYVSKFTMYE AI+E T NLS+ CKIGESVYKANI+G+VLAVK+ R+D +EELK
Sbjct 239 LSGVSGYVSKFTMYEIDAMEGTNLSDNCKIGESVYKANIDGRVLAVKKIKKASEELK 296

Query 352 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLSEELFAKSCSETSNRSRTLTWCOR 411
ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLSEELF++S +TSNS SLTW GR
Sbjct 299 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLSEELFSEB-SKTSNSVSVLTSWGR 357

Query 412 ISIAVDVSMGLQYMERHAYPRIVHRDITSSNLLDSNFKAKIANFSGMARTFNNPMKKID 471
++IA+DV++GLQYMERH YPRI+HRDIT+SNLL SNFKAKIANF MART TN MM KID
Sbjct 358 ITIAMDVAIGLQYMERHYPRIIHRDITTSNLLDSNFKAKIANFGMARTSNMMPKID 417

Query 472 VFAFGVLLIELLTGKRAMTTKENGSEVVMKMDIKWIFDQENREERLRKMDPKLDNYP 531
VFAFGVLLIELLTG+KAMTTKENGSEV+LMD KRIID E NREERLRKMDPKL++Y+P
Sbjct 418 VFAFGVLLIELLTGKAMTTKENGSEVVLKMDKFWKIFDLEGNREERLRKMDPKLESFYP 477

Query 532 IDVALSIAS 540
ID ALSIAS
Sbjct 478 IDVALSIAS 486

```

>emb|CA002941.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
>emb|CA002970.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=487

Score = 722 bits (1863), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 350/489 (71%), Positives = 412/489 (84%), Gaps = 4/489 (0%)

```

Query 53 YIQSGPNFLSITSVSNIFDPSLSTARASNLQHEEDKLIPQVLLIPVTCCTGNRSGFAN 112
Sbjct 1 Y+QSGPNFLS++S+IP+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN 60
YRAQSGPNFLSISNIDITNPLSLPIAKASNIEADKRLPDQLLLVPVTCCTGNRSGFAN

Query 113 TSVEINQGSDFYFVATTLYQNLTNWHAVMDINPGLSQPTLPDPIGQVVIPLFCCKPSKNQL 172
+Y I GSD+P+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCCKPSKNQL
Sbjct 61 I+Y I GSD+P+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCCKPSKNQL 120
TSYIKQGNFTLSITSYQNLTNLYLFKNFNNPNSPTLLPLDTKVSVPFLFCCKPSKNQL

Query 173 DRGKYLITHVQNDVNSVFNKLGASQDILSENNGQNTAASNLPVLPVTLPLDL 232
+GIGYLIIT+VWQ DNV+ VS+K GAS ++L+ENN+ NPTA++N VLIPTV LP L
Sbjct 121 NKGIKYLITYVQNDNVTLVSSKFGASQVEMLAENN+-NFTASTNRSVLIPVTLPLK 178

Query 233 IQGSPSDGRKRI+GLPVIIGISLGCCTLLVVVSAILLVCCCLMKKSLNRSSAETAADKL 291
Q S+GRK L+IIGISIG ++V + IV V CLMK LNRS SS+ETADKL
Sbjct 179 DQPSNDRGRSSQNLALLIGISLGSAPFLLVLTLSLVVYVCLMKKSLNRSSAETAADKL 238

Query 292 LSGVSGYVSKFTMYETQALIAEMNLSEQCCKIGESVYKANIIGKVLAVKRFKEDYTEELK 351
LSGVSGYVSKFTMYE AI+E T NLS+ CKIGESVYKANI+G+VLAVK+ R+D +EELK
Sbjct 239 LSGVSGYVSKFTMYEIDAMEGTNLSDNCKIGESVYKANIDGRVLAVKKIKKASEELK 296

Query 352 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLSEELFAKSCSETSNRSRTLTWCOR 411
ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLSEELF++S +TSNS SLTW GR

```

Sbjct 299 ILQKVNHCNLIKVMGVSSDNDGNCFLVVEYAENGSLSEEWLFSB-SKTSNSVSVLTSWSGR 357
ILQKVNHCNLIKVMGVSSDNDGNCFLVVEYAENGSLSEEWLFSB-SKTSNSVSVLTSWSGR

Query 412 ISTAVDSMGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNPMMGKID 471
I+I+DV++GIQYMHAY YPRI+HRDIT+SNILL SNFKAKIANF MART TN MM KID

Sbjct 358 ITIAMCVAGIQYMHAYPRIHRDITSSNILLSDNFKAKIANFSMARTFNPMMGKID 417
ITIAMCVAGIQYMHAYPRIHRDITSSNILLSDNFKAKIANFSMARTFNPMMGKID

Query 472 VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP 531
VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP

Sbjct 418 VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP 477
VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP

Query 532 IDVALSLAS 540 47
ID ALSLA

Sbjct 478 IDVALSLAS 486 47
IDVALSLAS

>emb|CAO02966.1| LysM-domain containing receptor-like kinase [Medicago tornata]
Length=467

Score = 718 bits (1853), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 349/489 (71%), Positives = 411/489 (84%), Gaps = 4/489 (0%)

Query 53 YIQSPNPLSLTSVSNITDTPSLISARASNLQHEEDKLIPQGVLLIPVTCGCTGNRNFAN 112
Y IQSPNPLSLTSVSNITDTPSLISARASNLQHEEDKLIPQGVLLIPVTCGCTGNRNFAN

Sbjct 1 YRAQSPNPLSLTSVSNITDTPSLISARASNLQHEEDKLIPQGVLLIPVTCGCTGNRNFAN 60
YRAQSPNPLSLTSVSNITDTPSLISARASNLQHEEDKLIPQGVLLIPVTCGCTGNRNFAN

Query 113 ISVEINQDSFYVATTIYQNLNHWAMDLNPLSQFTLPIGIQVPLPCKCPKSNKOL 172
I+Y I CD+Y++T YQNLN+ ++ NP LS LP+ +V +PLFCCKPKSNKOL

Sbjct 61 ITYSIKLQDNFTILSTYSQNLNHWAMDLNPLSQFTLPIGIQVPLPCKCPKSNKOL 120
ITYSIKLQDNFTILSTYSQNLNHWAMDLNPLSQFTLPIGIQVPLPCKCPKSNKOL

Query 173 DRGKYLITHWQPNDSVFSNKLGAQPDLSENNGYQNTFAASNLVPLVLTLPOL 232
+GIKYLT+HWQ NDNV VSK GAS ++L+ENNA+ NFTH+N VLIPTV LP L

Sbjct 121 NKGILYLT+HWQPNDSVFSNKLGAQPDLSENNGYQNTFAASNLVPLVLTLPOL 178
NKGILYLT+HWQPNDSVFSNKLGAQPDLSENNGYQNTFAASNLVPLVLTLPOL

Query 233 IQSPSDGRKHRI-GLPVIIGISLGLTLLVWVAAIL-LVCVCCKIRKMSARSASSAETA 291
S+GRK L +IIIGISL +V +LV V CLMK LNRS SS+ETADKL

Sbjct 179 IQSPSDGRKHRI-GLPVIIGISLGLTLLVWVAAIL-LVCVCCKIRKMSARSASSAETA 238
IQSPSDGRKHRI-GLPVIIGISLGLTLLVWVAAIL-LVCVCCKIRKMSARSASSAETA

Query 292 ISGVSGVSKPTMYETGAILEATMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTEEL 351
ISGVSGVSKPTMYE AI+E TMLNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK

Sbjct 293 ISGVSGVSKPTMYEIDAMTGMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTEEL 298
ISGVSGVSKPTMYEIDAMTGMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTEEL

Query 352 ILQKVNHCNLIKVMGVSSDNDGNCFLVVEYAENGSLSEEWLFSB-SKTSNSVSVLTSWSGR 411
ILQKVNHCNLIKVMGVSSDNDGNCFLVVEYAENGSLSEEWLFSB-SKTSNSVSVLTSWSGR

Sbjct 299 ILQKVNHCNLIKVMGVSSDNDGNCFLVVEYAENGSLSEEWLFSB-SKTSNSVSVLTSWSGR 357
ILQKVNHCNLIKVMGVSSDNDGNCFLVVEYAENGSLSEEWLFSB-SKTSNSVSVLTSWSGR

Query 412 ISTAVDSMGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNPMMGKID 471
I+I+DV++GIQYMHAY YPRI+HRDIT+SNILL SNFKAKIANF MART TN MM KID

Sbjct 358 ITIAMCVAGIQYMHAYPRIHRDITSSNILLSDNFKAKIANFSMARTFNPMMGKID 417
ITIAMCVAGIQYMHAYPRIHRDITSSNILLSDNFKAKIANFSMARTFNPMMGKID

Query 472 VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP 531
VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP

Sbjct 418 VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP 477
VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP

Query 532 IDVALSLAS 540 47
ID ALSLA

Sbjct 478 IDVALSLAS 486 47
IDVALSLAS

>dbj|BAI79275.1| LysM type receptor kinase [Lotus japonicus]

>dbj|BAI79285.1| LysM type receptor kinase [Lotus japonicus]

Length=591

GENE ID: 100380877 Lys11 | LysM type receptor kinase [Lotus japonicus]
(10 or fewer PubMed links)

Score = 706 bits (1823), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 370/606 (61%), Positives = 462/606 (76%), Gaps = 24/606 (3%)

Query 1 MAVFEVSLTGAQILVYVLMFFTC---IEAQSOQNTGNFSCPSNPPSCCTVYTIYSOS 57
M FE+ + ++MFE+ I AQ TNGTNFSCD +SPSCC+TVTYT +QS

Sbjct 1 MTFSEF---FTNTFLALNMFSTTHHILAQLSHTNGNFGSCPDVSPSCCTVYTYFAGS 57
MTFSEF---FTNTFLALNMFSTTHHILAQLSHTNGNFGSCPDVSPSCCTVYTYFAGS

Query 58 NPLSLTSVSNITDTPSLISARASNLQHEEDKLIPQGVLLIPVTCGCTGNRNFANIGYE 117
NPLSLTSVSNITDTPSLISARASNLQHEEDKLIPQGVLLIPVTCGCTGNRNFANIGYE

Sbjct 58 NPLSLTSVSNITDTPSLISARASNLQHEEDKLIPQGVLLIPVTCGCTGNRNFANIGYE 117
NPLSLTSVSNITDTPSLISARASNLQHEEDKLIPQGVLLIPVTCGCTGNRNFANIGYE

Query 118 NQGDSEFYVATTIYQNLNHWAMDLNPLSQFTLPIGIQVPLPCKCPKSNKOLDRGK 177
+G+S+Y++T YNLNWN V D NP ++ LP+GI+VWPLPCKCPKPS L+GI+Q
KEGESYIYLTSTSYENLNWETVQDSNPYNYFLLPVGKIVPLPCKCPKSNYHLNKGIE

Sbjct 118 NQGDSEFYVATTIYQNLNHWAMDLNPLSQFTLPIGIQVPLPCKCPKSNKOLDRGK 177
NQGDSEFYVATTIYQNLNHWAMDLNPLSQFTLPIGIQVPLPCKCPKSNYHLNKGIE

Query 178 YLT+HWQPNDSVFSNKLGAQPDLSENNGYQNTFAASNLVPLVLTLPOLIQSP 236
YLT+HWQ NDNVS V+K G S QOI+SENN+ QNTFAA+N P+LPIPTV LP L QS

Sbjct 178 YLT+HWQPNDSVFSNKLGAQPDLSENNGYQNTFAASNLVPLVLTLPOLIQSP 237
YLT+HWQPNDSVFSNKLGAQPDLSENNGYQNTFAASNLVPLVLTLPOLIQSP

Query 237 SDGRKHRI-GLPVIIGISLGLTLLVWVAAIL-LVCVCCKIRKMSARSASSAETA-DKLL 292
S+GRK L +IIIGISL +V +LV V CLM LNRS SS+ETADKL

Sbjct 237 SDGRKHRI-GLPVIIGISLGLTLLVWVAAIL-LVCVCCKIRKMSARSASSAETA-DKLL 297
SDGRKHRI-GLPVIIGISLGLTLLVWVAAIL-LVCVCCKIRKMSARSASSAETA-DKLL

Query 293 ISGVSGVSKPTMYETGAILEATMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTEEL 352
ISGVSGVSKPTMYE I+EAT+NL+EQCKIGESVYKANI+G+VLAVK+ KEDVTEE+ I

Sbjct 293 ISGVSGVSKPTMYEIDAMTGMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTEEL 357
ISGVSGVSKPTMYEIDAMTGMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTEEL

Query 353 ILQKVNHCNLIKVMGVSSDNDGNCFLVVEYAENGSLSEEWLFSB-SKTSNSVSVLTSWSGR 412
ILQKVNHCNLIKVMGVSSDNDGNCFLVVEYAENGSLSEEWLFSB-SKTSNSVSVLTSWSGR

Sbjct 358 ILQKVNHCNLIKVMGVSSDNDGNCFLVVEYAENGSLSEEWLFSB-SKTSNSVSVLTSWSGR 413
ILQKVNHCNLIKVMGVSSDNDGNCFLVVEYAENGSLSEEWLFSB-SKTSNSVSVLTSWSGR

Query 413 ISTAVDSMGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNPMMGKID 471
I+I+DV++GIQYMHAY YPRI+HRDIT+SNILL SDNFKAKIANF SMART NPM+ K+DV

Sbjct 414 ISTAVDSMGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNPMMGKID 472
ISTAVDSMGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNPMMGKID

Query 473 VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP 532
P+GVVL+ELL+G+K+T N E+ I +FD +E REER+R+MDER++ YPI

Sbjct 474 VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP 536
VFAGVGVLEILLTGKAMTTKENGSEVVMWMDKIWKIDQENREERLRKMDPKLNNYP

Query 533 IDVALSLASLAVNCTADKSLRPTAEVLISLIL-LTPQSPATLERSLTSGLDVEATQIV 591
D ALSLA L+ACT+K LSRPT+ E+VLISLIL TQ SP TERS Y GIDV+ Y++

Sbjct 527 DDALSLAFIAMNCTSEKPLSRPTMGHVVLISLLMTQHSPTTLERSGWT-CGLDWDVTVMQ 585
 Query 532 TSISAR 597
 T I A R
 Sbjct 586 TLIAAR 591

>ref|XP_002269472.1| **NC** PREDICTED: hypothetical protein [Vitis vinifera]
 enb|CBII17584.3| **E** unnamed protein product [Vitis vinifera]
 Length=590

GENE ID: 100259809 LOC100259809 | hypothetical protein LOC100259809
 [Vitis vinifera] (10 or fewer PubMed links)

Score = 643 bits (1659), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 329/575 (57%), Positives = 420/575 (73%), Gaps = 6/575 (1%)

Query 25 IFAQSQQTNGTNGFPCSPNSPPSCETVYVYISQSPNLSLTGVSNIQDTSPLSTARASNIQ 84
 I AQS T TNPSC +8P SC+TVV Y +Q+P FL + +8+P F S LIA ASNI
 Sbjct 20 IFAQSPATVFNISCTDTSFASQQTYYVYAAQAPGLDVGNIISDLFGISKLSIAEASNIA 79
 Query 85 HEEDKLIPGOVLLIPVTCCTGCTGNRSFANISYEINQDSFYFVATTIYQNLINWHAWMIDN 144
 EE +L + Q+LLP+ C CTGN FAN I+Y I GSYFY+T + +NLN+AV LN
 BEFAALSGPQVLLIPVTCCTGCTGNRSFANISYEINQDSFYFVATTIYQNLINWHAWMIDN 139
 Query 145 PQLSQFTLPIGTQVPLPCKCKPSKNDLGKYLITVWQPNWVNSVFNKLGASPDQI 204
 PQL TL +Q+VV PLCKCKPSK+ D+GI YLIT+VWQF D+V V L ASP DI
 Sbjct 140 PQLSEPTLQGVQEVVPLPCKCKPSKNSDKGINLITYWQPGDVLVGTNKLKASFDVI 199
 Query 205 LSENNYQNTFAASNLPVLIPVTLPLDPLQISPDGRKHRIGLVIGISGLCTLLVWSA 264
 ENN NFA+ + PVLIPV+ P L Q K R L + + + S G L + + +
 Sbjct 200 RUENN-NLAFASQDVPLIPVQSPFLLTQFERRASGRWILALVL--STGALLIFLIVS 256
 Query 265 ILIVGVCCIMKSLNRSASAEATD--KLLSGVSGVSKPTMYTGATLATNLSQCK 322
 + + K + + S SS E T D KLL GVG+ K P MYET + IADNML+E +
 Sbjct 257 ILVVTGLIKKKTLDBSSSELETTDLKILPGVSGYLGKPIMYETKIMEATNMLNEHYR 316
 Query 323 IGESVYKNIKGKVLAVKRFKEDVTEELKILQVNHGNILVKMGVSSDNDGCVFYVEYA 382
 IG SVY+ A I G+V+AVK+ KED+TEEL+ILQVNHGNILVKMGVSSD DON F+VEYA
 Sbjct 317 IGGSVYRATINGQVAVKTKEDITEELKILQVNHGNILVKMGVSSDADGRFLVVEYA 376
 Query 383 ENGSLLEWLFKASCSETSNSRTSLTWQRISIAVDVMGLQYMHAYPRIVRHDTSSN 442
 ILLEWLF+M L R S +8+ LTM QRI +A+DV+ GLQYMH E +VHRDI + +N
 Sbjct 377 ENGSLWLMFKPSPSSSEV+ATLDRGRQVALLVWANGLYMHESTQPVVHRDIANN 435
 Query 443 ILLDSNFRKAIANSMTATFNPMNSKIDVAFVGLVLELLTGKRAMTKENGVEVLMK 502
 ILLDS FRKAIANSMA N M K +DVAFVGLV+ELL+G+KAM + NGE+VLMK
 Sbjct 436 ILLDSRFRKAIANSMTATFNPMNSKIDVAFVGLVLELLSGKKAMQMRANGEVLMK 495
 Query 503 DIWKIFDOENREERLRKMDPKLONYPIIDYALSLASLVNCTADKLSRPTIAEIVLS 562
 DI +I + E+ RE+R+RMDP L+N+Y P D AL+LA LA +CT +KS +R+AEI +
 Sbjct 496 DIWEILEVDKREDRINWMDPLNFYFDGALNLAGLANSCTCKSSASRMSAEIAPN 555
 Query 563 LSLTLQSPATLERSLTSGDVEATQIVTSISAR 597
 LSL+ + + S LERS T E QI+ T AR
 Sbjct 556 LSVLTQSPATLERSLTSGDEPEETIQIINPVIAR 590

>ref|XP_002533280.1| **S** serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 gb|EF29112.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 Length=620

GENE ID: 8272992 RCOM_0411680 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 618 bits (1594), Expect = 6e-175, Method: Compositional matrix adjust.
 Identities = 330/602 (54%), Positives = 420/602 (69%), Gaps = 32/602 (5%)

Query 23 TCIIEASQQTNGTNGFPCSPNSPPSCETVYVYISQSPNLSLTGVSNIQDTSPLSTARASNI 82
 T + AQS Q GTNFC + P C+TVV Y +Q PNL+L +S+P F S LIA ASN
 Sbjct 24 TYVTAQSPQ--GTNFCSDVLPSPCQTYYVYAAQPNFLNLGNISDLFVAKLSIASASN 81
 Query 83 LQHEEDKLIPGOVLLIPVTCCTGCTGNRSFANISYEINQDSFYFVATTIYQNLINWHAWMIDN 142
 LE E +L + Q+LLP+ C CTGN FAN I+Y I GDSFYFV+T + +NL M AV
 Sbjct 82 IVEDEIPFQVLLIPVTCCTGCTGNRSFANISYEINQDSFYFVATTIYQNLINWHAWMIDN 141
 Query 143 IIMPQLSQFTLPIGTQVPLPCKCKPSKNDLGKYLITVWQPNWVNSVFNKLGASPDQI 202
 NP L L G +VV PLCKCKPSK+ G I+YLIT+VWQF D+ + V K ASP
 Sbjct 142 IENPNDPLTLHPGDQVPLPCKCKPSKNDKHKYQYLITVWQPEDDIFKVGKFNASPH 201
 Query 203 DILSENNYQNTFAASNLPVLIPVTLPLDPLQISPDGRKHRIGLVIGISGLCTLLVW 261
 DI +NNY +P+ A + P+LIPV +P L Q SPS + + L +II S+ LL+
 Sbjct 202 DIAIQNNY--DFTAVHPLIPVTLIPVTPILSPSPSPFQSRHLLIVITVSAGALLIF 260
 Query 262 VSAIILV--QVCLMK--SLNRSASAEATD--KLLSGVS + DKL GVS 296
 V + + C C K + + +R+ S E T KLL GVS
 Sbjct 261 LVLAVLVHAKSCSKKKKMTLHRNSCLETTDLQIKQGYKRSFEKIIQDKLLPGVS 320
 Query 297 GYVSKPTMYTGATLATNLSQCKIGESVYKNIKGKVLAVKRFKEDVTEELKILQV 356
 GY+ K MY+ IL AT+L E +IG SVY+ANT G+VIAV+ K D+TEEL ILQV
 Sbjct 321 GYLGKPIMYDKEITLATMDLHEHYRIGGSVYRANINGQVLAVKTRVDITTEELNILQV 380
 Query 357 NRGNIIVKMGVSSDNDGCVFYVEYAEAGSLLEWLFKASCSETSNSRTSLTWQRISIAV 416
 NH NIVKMG+SS+ DG+C+FYAEAGSL+WL K + +8+ L+W QR+ IA+
 Sbjct 381 NRGNIIVKMGVSSDNDGCVFYVEYAEAGSLLEWLFKASCSETSNSRTSLTWQRISIAV 439
 Query 417 DVMGLQYMHAYPRIVRHDTSSNILLDSFRKAIANSMTATFNPMNSKIDVAFVGLVLELL 476
 DV+ GLQYMH E P +VR DI +SNILLDS FRKAIANS+T M+ K+DVAFG
 Sbjct 440 DVASGLQYMHAYPRIVRHDTSSNILLDSFRKAIANSMTATFNPMNSKIDVAFVGLVLELL 499
 Query 477 VVLEILLTGKRAMTKENGVEVLMKDIWKIFDOENREERLRKMDPKLONYPIIDYAL 536
 VVLEILL G+KAM T ENGE+V+LNR+ + + E RERL+MDP L+N+YPID AL
 Sbjct 500 VVLEILLGKRAMTKENGVEVLMKDIWKIFDOENREERLRKMDPKLONYPIIDYAL 559

Query 537 SLASLAVNCTADKSLRPTAIVLSILLTQSPATLERSLTSGLDVEA-TQIVTSIS 595
 Sbjct 560 SLANLARCTLEKSSARFMAEIVFNLTVLTSQCSLETLRGWT-SGLEAEEDIQITSPVI 618

Query 596 AR 597
 AR
 Sbjct 619 AR 620

>ref|XP_002310199.1| [G] predicted protein [Populus trichocarpa]

gb|EEE90648.1| [G] predicted protein [Populus trichocarpa]
 Length=661

GENE ID: 7473142 POPTRDRAFT_870366 | hypothetical protein [Populus trichocarpa]
 (10 or fewer PubMed links)

Score = 595 bits (1534), Expect = 7e-168, Method: Compositional matrix adjust.
 Identities = 321/607 (70%), Positives = 421/607 (70%), Gaps = 16/607 (2%)

Query 1 MAVFVSLTLAGQILLVVMFFTCIAAQSQQTNGTNFSCPSNPPSCCTVYVYISQSPNF 60
 MA + + K + + V + + L + P + + + G T N F S C P S P S C T V Y + V + + P + P
 Sbjct 1 MAISLLSSFTQALFFVLVFFSTY-VTAQAPGCTNFCPSVDSPSTCTPYISYLAQPPDF 59

Query 61 LSLTSVSNIFDTPSLIARASNLOHREDKLPQGVLLIPVTCGCTGNRSFANISYEINQ 120
 L L L + S + + F S I A A R N L E + L P Q I L L + P C C T G + + S F N I + Y I G
 Sbjct 60 LLDGKLSHLPISRTLIASASNVSEDTPLFFNQILLVPIRCGCTGSGSFVNITQIQGG 119

Query 121 DSYFYVATTIYQNLTNWAVMDLNPGLSQFTLPIGIQVVPFLCKCPKSNGLDRIKYL 180
 D S Y V + G T + V G T + F L C K C P S + L + G I + + L
 Sbjct 120 DSIYSVTSIFENLTNWRVLEAHSNLTPTLLHAGDEVIFFLCKCPKSNGLHLENGIHL 179

Query 181 TTVWQPNQDNVSFVSNKLAGSPQDILSENNYQNTAASNLPVLPVTLPLDILQ---SPS 237
 T + W Q P D + + V + L A S + + I + E N N Y N F A A P + I P V + L P L Q + P
 Sbjct 180 TTVWQPGDDLKKVAAMLNASENVIENNY-DNFNAVYVFPVPSKLPVLSQPYLTPE 238

Query 238 D-GRRKRIQLPVIIGISGLTLLV-VAAILLVCCCLK-MKSLNRRASAETAD--KLL 292
 G K H V I + S + + + A L + C K K + L + R + S E T + D K I L L
 Sbjct 239 KRSGKIL--WIVVAIDASTFTTCLPAFLHRCRSYKATKALDRTCELETSPODKLL 296

Query 293 SGVSFVSKPTMYETGAILEATMNLSEQCKIGESVYKANIIGKVLAVKRKEDVTEELKI 352
 S + + + K + + V + I + S + + T M + L E K I G S V Y A N I G V L A V K + R + D V T E E L K I
 Sbjct 297 PGVLGDLKSIYIEVKALMEGTMDLHEHYKIGSVYRANINGCVLAVKKTDDVTEELKI 356

Query 353 LQKVNRCNIAVKLMGSSDND--GNCFFVVEYAENGSLERLWFAKSCSETSNRSRLTWQ 410
 L Q K V + H N I V K L M G + S S + D G N F + V V E Y A E N G S L + W L K S + S + B I W Q
 Sbjct 357 LQKSHANIAVKLMGMSSEGDREGRNLFVVEYAENGSLDKWLHFS--EBSSSSVGLFWKQ 415

Query 411 RITSIAVOMGQVMIEHAYPRIVIRIDITSSNILLSDNFKAKIANTPMARTFNMMSKRI 470
 R + + F A + + G I G V S + D I + S N I L L S + A K I A N T P M A R T + M M K
 Sbjct 416 RMQVQDVANGQVLTLEHTQPTVTHKIDRTSNILLSTFRAKIANTSMARAATDSMMKPD 475

Query 471 DVYFAGVGLTIRKANKMTKENGVEVMKDKMKIPQKQENREERLRKMDPLKNLY 530
 D V F P G V L + E L L + G + K M T K E G E + V + L + + I + + E E R E E R L R K M D P L N Y
 Sbjct 476 DVDFPGVGLLWLGKKAMVTKEGEVLILLCREIKDVLMEERERLRKMDPLNRY 535

Query 531 PTDALSLASLAVNCTADKSLRPTAIVLSILLTQSPATLERSLTSGLDVEATQI 590
 P I D + S L A + L A C T + K S R P + A E I V + L + I T Q S P T L E R T S + T + +
 Sbjct 536 PIDSAMSLATLARCTLEKSSARFMAEIVFNLTVLTSQCSLETLRGWT-SGLEAEEDITRL 594

Query 591 VTISAR 597
 V + + A R
 Sbjct 595 VSPVTAR 601

>gb|ADJ19109.1| [G] truncated Nod-factor receptor 5A [Glycine max]
 Length=337

GENE ID: 100498058 NFR5A | Nod-factor receptor 5A [Glycine max]
 (10 or fewer PubMed links)

Score = 536 bits (1381), Expect = 4e-150, Method: Compositional matrix adjust.
 Identities = 277/337 (82%), Positives = 301/337 (89%), Gaps = 1/337 (0%)

Query 1 MAVFVSLTLAGQILLVVMFFTCIAAQSQQTNGTNFSCPSNPPSCCTVYVYISQSPNF 59
 MAVF L L L + Q I L + V + M F T I A Q R Q N N T N F S C P S + S P S C T V Y T Y I + Q S P N
 Sbjct 1 MAVFFFLPLSGLLCLVIMLFSTNIVAQSQQDNRTNFCPSDSFSPSCCTVYVYISQSPNF 59

Query 60 FLSTLSVSNIFDTPSLIARASNLOHREDKLPQGVLLIPVTCGCTGNRSFANISYEINQ 119
 F L S T L + S N I F D T P S L I A R A S N L O H R E D K L P G V L L I P V T C G C T G N R S F A N I S Y E I N Q
 Sbjct 61 FLSTLSNIFDTPSLIARASNLEPMDDKLVKQVLLIPVTCGCTGNRSFANISYEINQ 120

Query 120 DSYFYVATTIYQNLTNWAVMDLNPGLSQFTLPIGIQVVPFLCKCPKSNGLDRIKYL 179
 D S E F Y V A T T I Y + N L T N W A V M D L N P L S L P I G I Q V P L F C K P S K N G L D R I K Y L
 Sbjct 121 DSEFYVATTIYENLTNWRVMDLNPVSPNKLPIGQVVPFLCKCPKSNGLDKELKYL 180

Query 180 ITHWQPNQDNVSFVSNKLAGSPQDILSENNYQNTAASNLPVLPVTLPLDILQSPSDG 239
 I T + W + P D N V S + K G A S P + D I + S E N N Y Q N T A A N L P V L P V T L P L A R S P S D G
 Sbjct 181 ITHWQPNQDNVLSNRPASPEDINSENNYQNTAANNLPVLPVTLPLVARSFSDG 240

Query 240 RKRRTGLPVIIGISGLTLLVVAAILLVCCCLMKMSLNRRASAETADKLLSGVSGV 299
 R K + T P V I I G I S G L T L L V + A I L L V C L M K + M R S A S A E T A D K L L S G V S G V
 Sbjct 241 RKGGRIRLPIIGISGLTLLVLAIVLVVYVCLMKMTNRRASAETADKLLSGVSGV 300

Query 300 SKPTMYETGAILEATMNLSEQCKIGESVYKANIIGKVLAVKRKEDVTEELKI 336
 S K P T M Y E T A + E A T M N L S E Q C K I G E S V Y K A N I I G K V
 Sbjct 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIIGKVL 337

>dbj|BA085147.1| Nod factor receptor protein [Glycine soja]
 Length=337

Score = 519 bits (1337), Expect = 4e-145, Method: Compositional matrix adjust.
 Identities = 261/327 (79%), Positives = 285/327 (87%), Gaps = 1/327 (0%)

Query 5 FVSLTLAGQILLVVMFFTCIAAQSQQTNGTNFSCPSNPPSCCTVYVYISQSPNF 63
 F L L + Q I L + V + M F T I A Q S Q N N T N F S C P S + S P S C T V Y T Y I + Q S P N F L S L


```

Sbjct 1   FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNLFSL 60
Query 64   TSVSNIFDTSPLSIARASNLQHEEDKILPGQVLLIPVTCGCTGNRSFANISYEINQGDGF 123
          F++SNI+FDTSPLSIARASNL++DKL+ QVLL+PVTGCTGNRSFANISYEINQGDGF
Sbjct 61   TNISNIFDTSPLSIARASNLPMDDKILVKDQVLLIPVTCGCTGNRSFANTSYEINQGDGF 120
Query 124  YFVATTLYQNLTNRHVMNDINPGLSOFTLPIGIGVVPFLFCKCPSKNQLDRGIKYLITV 183
          YFVATT Y+NLTN+AVMDINP L$ LPIGIGVVP FLFCKCPSKNQLD+IKYLIT+V
Sbjct 121  YFVATTSYENLTNRHVMNDINPVLSPNKLPIGIGVVPFLFCKCPSKNQLDRGIKYLITV 180
Query 184  WQPNVNVSFVNKLGASPDILSENNYQGNFTAAANLPLVLPVTLPLDIQSPSDGRKRR 243
          W+P DNVS V$+K GASP+DI+SENNYQGNFTAA+NLPLVLPVT LP L +$P$DGRK
Sbjct 181  WKQPNVNVSIVBQKFGASPEDIMSENNYQGNFTAAANLPLVLPVTLPLVARSFSDGRKGG 240
Query 244  IGLPVITIGISGCTLLVVSAILLVCCCLMKMSINRSASSAETADKLLSGVSGYVSKPT 303
          I LPIVITIGISGCTLLV V A LLV V CLRMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241  IRLPVITIGITGCTLLVLVLVSIWAYGYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300
Query 304  MYETGAILLEATNNLSEQCKIGESVYKA 330
          MYET AI+EA+NNLSEQCKIGESVYKA
Sbjct 301  MYETDAIMEATNNLSEQCKIGESVYKA 327

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>dbj|BA085143.1| Nod factor receptor protein [Glycine soja]
>dbj|BA085149.1| Nod factor receptor protein [Glycine soja]
>dbj|BA085156.1| Nod factor receptor protein [Glycine soja]
11 more sequence titles

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>dbj|BA085159.1| Nod factor receptor protein [Glycine max]
>dbj|BA085160.1| Nod factor receptor protein [Glycine max]
>dbj|BA085161.1| Nod factor receptor protein [Glycine max]
>dbj|BA085162.1| Nod factor receptor protein [Glycine max]
>dbj|BA085165.1| Nod factor receptor protein [Glycine max]
>dbj|BA085168.1| Nod factor receptor protein [Glycine max]
>dbj|BA085171.1| Nod factor receptor protein [Glycine max]
>dbj|BA085174.1| Nod factor receptor protein [Glycine max]
>dbj|BA085177.1| Nod factor receptor protein [Glycine max]
>dbj|BA085179.1| Nod factor receptor protein [Glycine max]
>dbj|BA085180.1| Nod factor receptor protein [Glycine max]
Length=327

```

Score = 516 bits (1329), Expect = 3e-144, Method: Compositional matrix adjust.
 Identities = 267/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

```

Query 5   FVSLTLGAQILYVIMFF-TCIEAQSQGTNGTNFSCPSNSPFCSETTYVTYIAQSPNLFSL 63
          F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPSCSETTYVTYI+QSPNLFSL
Sbjct 1   FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNLFSL 60
Query 64   TSVSNIFDTSPLSIARASNLQHEEDKILPGQVLLIPVTCGCTGNRSFANISYEINQGDGF 123
          F++SNI+FDTSPLSIARASNL++DKL+ QVLL+PVTGCTGNRSFANISYEINQGDGF
Sbjct 61   TNISNIFDTSPLSIARASNLPMDDKILVKDQVLLIPVTCGCTGNRSFANTSYEINQGDGF 120
Query 124  YFVATTLYQNLTNRHVMNDINPGLSOFTLPIGIGVVPFLFCKCPSKNQLDRGIKYLITV 183
          YFVATT Y+NLTN+AVMDINP L$ LPIGIGVVP FLFCKCPSKNQLD+IKYLIT+V
Sbjct 121  YFVATTSYENLTNRHVMNDINPVLSPNKLPIGIGVVPFLFCKCPSKNQLDRGIKYLITV 180
Query 184  WQPNVNVSFVNKLGASPDILSENNYQGNFTAAANLPLVLPVTLPLDIQSPSDGRKRR 243
          W+P DNVS V$+K GASP+DI+SENNYQGNFTAA+NLPLVLPVT LP L +$P$DGRK
Sbjct 181  WKQPNVNVSIVBQKFGASPEDIMSENNYQGNFTAAANLPLVLPVTLPLVARSFSDGRKGG 240
Query 244  IGLPVITIGISGCTLLVVSAILLVCCCLMKMSINRSASSAETADKLLSGVSGYVSKPT 303
          I LPIVITIGISGCTLLV V A LLV V CLRMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241  IRLPVITIGITGCTLLVLVLVSIWAYGYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300
Query 304  MYETGAILLEATNNLSEQCKIGESVYKA 330
          MYET AI+EA+NNLSEQCKIGESVYKA
Sbjct 301  MYETDAIMEATNNLSEQCKIGESVYKA 327

```

```

>dbj|BA085152.1| Nod factor receptor protein [Glycine soja]
Length=327

```

Score = 516 bits (1328), Expect = 5e-144, Method: Compositional matrix adjust.
 Identities = 267/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

```

Query 5   FVSLTLGAQILYVIMFF-TCIEAQSQGTNGTNFSCPSNSPFCSETTYVTYIAQSPNLFSL 63
          F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPSCSETTYVTYI+QSPNLFSL
Sbjct 1   FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNLFSL 60
Query 64   TSVSNIFDTSPLSIARASNLQHEEDKILPGQVLLIPVTCGCTGNRSFANISYEINQGDGF 123
          F++SNI+FDTSPLSIARASNL++DKL+ QVLL+PVTGCTGNRSFANISYEINQGDGF
Sbjct 61   TNISNIFDTSPLSIARASNLPMDDKILVKDQVLLIPVTCGCTGNRSFANTSYEINQGDGF 120
Query 124  YFVATTLYQNLTNRHVMNDINPGLSOFTLPIGIGVVPFLFCKCPSKNQLDRGIKYLITV 183
          YFVATT Y+NLTN+AVMDINP L$ LPIGIGVVP FLFCKCPSKNQLD+IKYLIT+V
Sbjct 121  YFVATTSYENLTNRHVMNDINPVLSPNKLPIGIGVVPFLFCKCPSKNQLDRGIKYLITV 180
Query 184  WQPNVNVSFVNKLGASPDILSENNYQGNFTAAANLPLVLPVTLPLDIQSPSDGRKRR 243
          W+P DNVS V$+K GASP+DI+SENNYQGNFTAA+NLPLVLPVT LP L +$P$DGRK
Sbjct 181  WKQPNVNVSIVBQKFGASPEDIMSENNYQGNFTAAANLPLVLPVTLPLVARSFSDGRKGG 240
Query 244  IGLPVITIGISGCTLLVVSAILLVCCCLMKMSINRSASSAETADKLLSGVSGYVSKPT 303
          I LPIVITIGISGCTLLV V A LLV V CLRMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241  IRLPVITIGITGCTLLVLVLVSIWAYGYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300
Query 304  MYETGAILLEATNNLSEQCKIGESVYKA 330
          MYET AI+EA+NNLSEQCKIGESVYKA
Sbjct 301  MYETDAIMEATNNLSEQCKIGESVYKA 327

```

```

>dbj|BA085148.1| Nod factor receptor protein [Glycine soja]
Length=327

```

Score = 515 bits (1327), Expect = 5e-144, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

```

Query 5   FVSLTLGAQILYVIMFF-TCIEAQSQGTNGTNFSCPSNSPFCSETTYVTYIAQSPNLFSL 63

```

Sbjct 1 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPCSETTYVTYI+QSPNLFSL 60
 FPFPLPLHSQICLIVLMFSTNVAQSQQDNRTNFSCPSDSPPCSETTYVTYI+QSPNLFSL

Query 64 TSVSNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF 123
 T+SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGSDF

Sbjct 61 TNISNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF 120
 TNISNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF

Query 124 YFVATTLYQNLTNWRAVDNLPGLSQFTLPIGIQVVPFLFCKCPKSNQLDRIKYLITV 183
 YFVATT Y+NLTNW AVMDNLP LS LPIGIQVVP FLFCKCPKSNQLD+ IKYLIT+V

Sbjct 121 YFVATTSYENLTNWRRAVDNLPVLSNPKLPIGIVVFLFCKCPKSNQLDRIKYLITV 180
 YFVATTSYENLTNWRRAVDNLPVLSNPKLPIGIVVFLFCKCPKSNQLDRIKYLITV

Query 184 WKPNNDVSVFNKLGASPDILSENNYGNFTAAANL+L+PVL+PVL+POLI+SPSGRKR 243
 W+P DNVS V+K GASP+DI+SENNYGNFTAA+NL+L+PVL+PVL+POLI+SPSGRKR

Sbjct 181 WKPNNDVSVFNKLGASPDILSENNYGNFTAAANL+L+PVL+PVL+POLI+SPSGRKR 240
 WKPNNDVSVFNKLGASPDILSENNYGNFTAAANL+L+PVL+PVL+POLI+SPSGRKR

Query 244 IGLPVIIGISIGCTLLVVSAILLVCCCLMKMSINRSASAEADKLLSGVSGVSKPT 303
 I+L+PVIIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGVSKPT

Sbjct 241 IRLPVIIGISIGCTLLVVLAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300
 IRLPVIIGISIGCTLLVVLAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET A+EA+TMNLSEQCKIGESVYKA

Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
 MYETDAIMEATMNLSEQCKIGESVYKA

>dbj|BA085178.1| **E** Nod factor receptor protein [Glycine max]
 length=327

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
 (10 or fewer PubMed links)

Score = 514 bits (1325), Expect = 9e-144, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTGAQILYVIMFF+TCIAQSQQTNGTNFSCPSNSPPCSETTYVTYI+QSPNLFSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPCSETTYVTYI+QSPNLFSL

Sbjct 1 FPFPLPLHSQICLIVLMFSTNVAQSQQDNRTNFSCPSDSPPCSETTYVTYI+QSPNLFSL 60
 FPFPLPLHSQICLIVLMFSTNVAQSQQDNRTNFSCPSDSPPCSETTYVTYI+QSPNLFSL

Query 64 TSVSNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF 123
 T+SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGSDF

Sbjct 61 TNISNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF 120
 TNISNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF

Query 124 YFVATTLYQNLTNWRAVDNLPGLSQFTLPIGIQVVPFLFCKCPKSNQLDRIKYLITV 183
 YFVATT Y+NLTNW AVMDNLP LS LPIGIQVVP FLFCKCPKSNQLD+ IKYLIT+V

Sbjct 121 YFVATTSYENLTNWRRAVDNLPVLSNPKLPIGIVVFLFCKCPKSNQLDRIKYLITV 180
 YFVATTSYENLTNWRRAVDNLPVLSNPKLPIGIVVFLFCKCPKSNQLDRIKYLITV

Query 184 WKPNNDVSVFNKLGASPDILSENNYGNFTAAANL+L+PVL+PVL+POLI+SPSGRKR 243
 W+P DNVS V+K GASP+DI+SENNYGNFTAA+NL+L+PVL+PVL+POLI+SPSGRKR

Sbjct 181 WKPNNDVSVFNKLGASPDILSENNYGNFTAAANL+L+PVL+PVL+POLI+SPSGRKR 240
 WKPNNDVSVFNKLGASPDILSENNYGNFTAAANL+L+PVL+PVL+POLI+SPSGRKR

Query 244 IGLPVIIGISIGCTLLVVSAILLVCCCLMKMSINRSASAEADKLLSGVSGVSKPT 303
 I+L+PVIIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGVSKPT

Sbjct 241 IRLPVIIGISIGCTLLVVLAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300
 IRLPVIIGISIGCTLLVVLAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET A+EA+TMNLSEQCKIGESVYKA

Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
 MYETDAIMEATMNLSEQCKIGESVYKA

>dbj|BA085144.1| Nod factor receptor protein [Glycine soja]
 dbj|BA085145.1| Nod factor receptor protein [Glycine soja]
 length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 267/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTGAQILYVIMFF+TCIAQSQQTNGTNFSCPSNSPPCSETTYVTYI+QSPNLFSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPCSETTYVTYI+QSPNLFSL

Sbjct 1 FPFPLPLHSQICLIVLMFSTNVAQSQQDNRTNFSCPSDSPPCSETTYVTYI+QSPNLFSL 60
 FPFPLPLHSQICLIVLMFSTNVAQSQQDNRTNFSCPSDSPPCSETTYVTYI+QSPNLFSL

Query 64 TSVSNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF 123
 T+SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGSDF

Sbjct 61 TNISNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF 120
 TNISNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF

Query 124 YFVATTLYQNLTNWRAVDNLPGLSQFTLPIGIQVVPFLFCKCPKSNQLDRIKYLITV 183
 YFVATT Y+NLTNW AVMDNLP LS LPIGIQVVP FLFCKCPKSNQLD+ IKYLIT+V

Sbjct 121 YFVATTSYENLTNWRRAVDNLPVLSNPKLPIGIVVFLFCKCPKSNQLDRIKYLITV 180
 YFVATTSYENLTNWRRAVDNLPVLSNPKLPIGIVVFLFCKCPKSNQLDRIKYLITV

Query 184 WKPNNDVSVFNKLGASPDILSENNYGNFTAAANL+L+PVL+PVL+POLI+SPSGRKR 243
 W+P DNVS V+K GASP+DI+SENNYGNFTAA+NL+L+PVL+PVL+POLI+SPSGRKR

Sbjct 181 WKPNNDVSVFNKLGASPDILSENNYGNFTAAANL+L+PVL+PVL+POLI+SPSGRKR 240
 WKPNNDVSVFNKLGASPDILSENNYGNFTAAANL+L+PVL+PVL+POLI+SPSGRKR

Query 244 IGLPVIIGISIGCTLLVVSAILLVCCCLMKMSINRSASAEADKLLSGVSGVSKPT 303
 I+L+PVIIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGVSKPT

Sbjct 241 IRLPVIIGISIGCTLLVVLAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300
 IRLPVIIGISIGCTLLVVLAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET A+EA+TMNLSEQCKIGESVYKA

Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
 MYETDAIMEATMNLSEQCKIGESVYKA

>dbj|BA085170.1| Nod factor receptor protein [Glycine max]
 length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTGAQILYVIMFF+TCIAQSQQTNGTNFSCPSNSPPCSETTYVTYI+QSPNLFSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPCSETTYVTYI+QSPNLFSL

Sbjct 1 FPFPLPLHSQICLIVLMFSTNVAQSQQDNRTNFSCPSDSPPCSETTYVTYI+QSPNLFSL 60
 FPFPLPLHSQICLIVLMFSTNVAQSQQDNRTNFSCPSDSPPCSETTYVTYI+QSPNLFSL

Query 64 TSVSNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF 123
 T+SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGSDF

Sbjct 61 TNISNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF 120
 TNISNI+FDTSPLSIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQGSDF

Query 124 YFVATTLYQNLTNWRAVDNLPGLSQFTLPIGIQVVPFLFCKCPKSNQLDRIKYLITV 183
 YFVATT Y+NLTNW AVMDNLP LS LPIGIQVVP FLFCKCPKSNQLD+ IKYLIT+V

Sbjct 121 YFVATTSYENLTNWRRAVDNLPVLSNPKLPIGIVVFLFCKCPKSNQLDRIKYLITV 180
 YFVATTSYENLTNWRRAVDNLPVLSNPKLPIGIVVFLFCKCPKSNQLDRIKYLITV

Query 184 WQPDNVSVFVNKLGASPDILSENNYGNFTAAANLPLVLPVTLPLDILQSPDGRKRR 243
 W4P DNVSV V8+K GASPD+DI+SENNYGNFTAAANLPLVLPVTL LP L +SPDGRK
 Sbjct 181 WKPGDNVSVV8DKFGASPDIMSENNYGNFTAAANLPLVLPVTLPLVLRSPDGRKGG 240

Query 244 IGLPVIIGISIGCTLLVWVAAILLWCCCLMKMSINRSASAEADKLLSGVSGVSKPT 303
 I L PVIIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET AI+EA TMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085167.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVIMFPF-CIEAQSQGTNTNFSCPSNPPCETTYVTYIQSPNLFSL 63
 F L L +QIL +V+M P T I AQSQ N TNFSCPS+PPCETTYVTI+QSPNLFSL
 Sbjct 1 FFLPLRHSQICLIVIMLFSTNIVAQSQDQNTNFSCPSDPPCETTYVTYIAQSPNLFSL 60

Query 64 TSVSNIFDTSPLSIARASNL+QHEEDKLI PGQVLLIPVTOGCTGNRSFANISYEINQGSF 123
 T+SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGSF
 Sbjct 61 ANISNIFDTSPLSIARASNLPEMDKLVKQVLLIPVTOGCTGNRSFANISYEINQGSF 120

Query 124 YFVATTLYQNLNWRHVMDLNPGLSQFTLPIGIQVPIFLCKCPKSNQDLRGIKYLTIV 183
 YFVATT Y+NITNW AVMDINP LS LPIGIQV PLFCCKCPKSNQDL+ IKYLTIV
 Sbjct 121 YFVATTSYENLNNWRHVMDLNPLVLSNPKLPIGIVPFLFCCKCPKSNQDLRGIKYLTIV 180

Query 184 WQPDNVSVFVNKLGASPDILSENNYGNFTAAANLPLVLPVTLPLDILQSPDGRKRR 243
 W4P DNVSV V8+K GASPD+DI+SENNYGNFTAAANLPLVLPVTL LP L +SPDGRK
 Sbjct 181 WKPGDNVSVV8DKFGASPDIMSENNYGNFTAAANLPLVLPVTLPLVLRSPDGRKGG 240

Query 244 IGLPVIIGISIGCTLLVWVAAILLWCCCLMKMSINRSASAEADKLLSGVSGVSKPT 303
 I L PVIIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET AI+EA TMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085164.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVIMFPF-CIEAQSQGTNTNFSCPSNPPCETTYVTYIQSPNLFSL 63
 F L L +QIL +V+M P T I AQSQ N TNFSCPS+PPCETTYVTI+QSPNLFSL
 Sbjct 1 FFLPLRHSQICLIVIMLFSTNIVAQSQDQNTNFSCPSDPPCETTYVTYIAQSPNLFSL 60

Query 64 TSVSNIFDTSPLSIARASNL+QHEEDKLI PGQVLLIPVTOGCTGNRSFANISYEINQGSF 123
 T+SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGSF
 Sbjct 61 TNISNIFDTSPLSIARASNLPEMDKLVKQVLLIPVTOGCTGNRSFANISYEINQGSF 120

Query 124 YFVATTLYQNLNWRHVMDLNPGLSQFTLPIGIQVPIFLCKCPKSNQDLRGIKYLTIV 183
 YFVATT Y+NITNW AVMDINP LS LPIGIQV PLFCCKCPKSNQDL+ IKYLTIV
 Sbjct 121 YFVATTSYENLNNWRHVMDLNPLVLSNPKLPIGIVPFLFCCKCPKSNQDLRGIKYLTIV 180

Query 184 WQPDNVSVFVNKLGASPDILSENNYGNFTAAANLPLVLPVTLPLDILQSPDGRKRR 243
 W4P DNVSV V8+K GASPD+DI+SENNYGNFTAAANLPLVLPVTL LP L +SPDGRK
 Sbjct 181 WKPGDNVSVV8DKFGASPDIMSENNYGNFTAAANLPLVLPVTLPLVLRSPDGRKGG 240

Query 244 IGLPVIIGISIGCTLLVWVAAILLWCCCLMKMSINRSASAEADKLLSGVSGVSKPT 303
 I L PVIIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYE AI+EA TMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085151.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 514 bits (1324), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVIMFPF-CIEAQSQGTNTNFSCPSNPPCETTYVTYIQSPNLFSL 63
 F L L +QIL +V+M P T I AQSQ N TNFSCPS+PPCETTYVTI+QSPNLFSL
 Sbjct 1 FFLPLRHSQICLIVIMLFSTNIVAQSQDQNTNFSCPSDPPCETTYVTYIAQSPNLFSL 60

Query 64 TSVSNIFDTSPLSIARASNL+QHEEDKLI PGQVLLIPVTOGCTGNRSFANISYEINQGSF 123
 T+SNIF+TSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGSF
 Sbjct 61 TNISNIFDTSPLSIARASNLPEMDKLVKQVLLIPVTOGCTGNRSFANISYEINQGSF 120

Query 124 YFVATTLYQNLNWRHVMDLNPGLSQFTLPIGIQVPIFLCKCPKSNQDLRGIKYLTIV 183
 YFVATT Y+NITNW AVMDINP LS LPIGIQV PLFCCKCPKSNQDL+ IKYLTIV
 Sbjct 121 YFVATTSYENLNNWRHVMDLNPLVLSNPKLPIGIVPFLFCCKCPKSNQDLRGIKYLTIV 180

Query 184 WQPDNVSVFVNKLGASPDILSENNYGNFTAAANLPLVLPVTLPLDILQSPDGRKRR 243
 W4P DNVSV V8+K GASPD+DI+SENNYGNFTAAANLPLVLPVTL LP L +SPDGRK
 Sbjct 181 WKPGDNVSVV8DKFGASPDIMSENNYGNFTAAANLPLVLPVTLPLVLRSPDGRKGG 240

Query 244 IGLPVIIGISIGCTLLVWVAAILLWCCCLMKMSINRSASAEADKLLSGVSGVSKPT 303
 I L PVIIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYE AI+EA TMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085146.1| Nod factor receptor protein [Glycine soja]

Length=327

Score = 514 bits (1324), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILVYVIMFP-TCIAEQSQGTNTNFSCPSNSPPSCETTYVTYISQSNFNL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPSCETTYVTYI+QSNFNL
 Sbjct 1 FPFLLPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFSCPSDPSPPSCETTYVTYIAQSNFNL 60

Query 64 TSVSNIFDTSPLSIARASNQHEEDKLI PQGVLLI PVTCGCTGNRSFANISYEINQGDGF 123
 T+SNIFDTSPLSIARASNLI+ +DKL+ QVLLI+PVTCGCTGNRSFANISYEINQGDGF
 Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLI PVTCGCTGNRSFANISYEINQGDGF 120

Query 124 YFVATTLQNLTNNHRAVMDLNPGLSQFTLP IGIQVVPFLFCKCPKSNQLDRGIKYLITV 183
 YFVATT Y+NTNN HRAVMDLNP IGIQVVP FLFCKCPKSNQLD+ IKYLITV
 Sbjct 121 YFVATTSYENLTNNRAVMDLNPGLSPNKLPIGIQVVPFLFCKCPKSNQLDKELIKYLITV 180

Query 184 WKPNQNVSVFNKLGASPDQILSENNYGNFTAAANLPLVLPVTLPLDQSPSGDRKKR 243
 W+P DNVS V8+K GASP+DI+SENNYGNFTAA+NLPLVLPVTL P L L +SPSGDRK
 Sbjct 181 WKPNQNVSLVSDKFGASPDIMSENNYGNFTAAANLPLVLPVTLPLVARSFSDGRKGG 240

Query 244 IGLPVIGISIGCTLLVVSAILLVCCCLMKMSINRSASSAETADKLLSGVSGVSKPT 303
 I LPIVIGISIGCTLLV+V A+LLV V CLMK+LNRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPLVIGISIGCTLLVLLVAVLLVYVYCLMKTLNRSASSAETADKLLSGVSGVSKPT 300

Query 304 MYETGAILLEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085153.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 514 bits (1323), Expect = 2e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILVYVIMFP-TCIAEQSQGTNTNFSCPSNSPPSCETTYVTYISQSNFNL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPSCETTYVTYI+QSNFNL
 Sbjct 1 FPFLLPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFSCPSDPSPPSCETTYVTYIAQSNFNL 60

Query 64 TSVSNIFDTSPLSIARASNQHEEDKLI PQGVLLI PVTCGCTGNRSFANISYEINQGDGF 123
 T+SNIFDTSPLSIARASNLI+ +DKL+ QVLLI+PVTCGCTGNRSFANISYEINQGDGF
 Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLI PVTCGCTGNRSFANISYEINQGDGF 120

Query 124 YFVATTLQNLTNNHRAVMDLNPGLSQFTLP IGIQVVPFLFCKCPKSNQLDRGIKYLITV 183
 YFVATT Y+NTNN HRAVMDLNP IGIQVVP FLFCKCPKSNQLD+ IKYLITV
 Sbjct 121 YFVATTSYENLTNNRAVMDLNPGLSQFTLP IGIQVVPFLFCKCPKSNQLDKELIKYLITV 180

Query 184 WKPNQNVSVFNKLGASPDQILSENNYGNFTAAANLPLVLPVTLPLDQSPSGDRKKR 243
 W+P DNVS V8+K GASP+DI+SENNYGNFTAA+NLPLVLPVTL P L L +SPSGDRK
 Sbjct 181 WKPNQNVSLVSDKFGASPDIMSENNYGNFTAAANLPLVLPVTLPLVARSFSDGRKGG 240

Query 244 IGLPVIGISIGCTLLVVSAILLVCCCLMKMSINRSASSAETADKLLSGVSGVSKPT 303
 I LPIVIGISIGCTLLV+V A+LLV V CLMK+LNRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPLVIGISIGCTLLVLLVAVLLVYVYCLMKTLNRSASSAETADKLLSGVSGVSKPT 300

Query 304 MYETGAILLEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085158.1| Nod factor receptor protein [Glycine max]
 Length=327

GENE ID: 100301877 *nfa55* | Nod factor receptor protein [Glycine max]
 (10 or fewer PubMed links)

Score = 514 bits (1323), Expect = 2e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILVYVIMFP-TCIAEQSQGTNTNFSCPSNSPPSCETTYVTYISQSNFNL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPSCETTYVTYI+QSNFNL
 Sbjct 1 FPFLLPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFSCPSDPSPPSCETTYVTYIAQSNFNL 60

Query 64 TSVSNIFDTSPLSIARASNQHEEDKLI PQGVLLI PVTCGCTGNRSFANISYEINQGDGF 123
 T+SNIFDTSPLSIARASNLI+ +DKL+ QVLLI+PVTCGCTGNRSFANISYEINQGDGF
 Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLI PVTCGCTGNRSFANISYEINQGDGF 120

Query 124 YFVATTLQNLTNNHRAVMDLNPGLSQFTLP IGIQVVPFLFCKCPKSNQLDRGIKYLITV 183
 YFVATT Y+NTNN HRAVMDLNP IGIQVVP FLFCKCPKSNQLD+ IKYLITV
 Sbjct 121 YFVATTSYENLTNNRAVMDLNPGLSPNKLPIGIQVVPFLFCKCPKSNQLDKELIKYLITV 180

Query 184 WKPNQNVSVFNKLGASPDQILSENNYGNFTAAANLPLVLPVTLPLDQSPSGDRKKR 243
 W+P DNVS V8+K GASP+DI+SENNYGNFTAA+NLPLVLPVTL P L L +SPSGDRK
 Sbjct 181 WKPNQNVSLVSDKFGASPDIMSENNYGNFTAAANLPLVLPVTLPLVARSFSDGRKGG 240

Query 244 IGLPVIGISIGCTLLVVSAILLVCCCLMKMSINRSASSAETADKLLSGVSGVSKPT 303
 I LPIVIGISIGCTLLV+V A+LLV V CLMK+LNRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPLVIGISIGCTLLVLLVAVLLVYVYCLMKTLNRSASSAETADKLLSGVSGVSKPT 300

Query 304 MYETGAILLEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085172.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 514 bits (1323), Expect = 2e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILVYVIMFP-TCIAEQSQGTNTNFSCPSNSPPSCETTYVTYISQSNFNL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPSCETTYVTYI+QSNFNL
 Sbjct 1 FPFLLPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFSCPSDPSPPSCETTYVTYIAQSNFNL 60

Query 64 TSVSNIFDTSPLSIARASNQHEEDKLI PQGVLLI PVTCGCTGNRSFANISYEINQGDGF 123
 T+SNIFDTSPLSIARASNLI+ +DKL+ QVLLI+PVTCGCTGNRSFANISYEINQGDGF

Sbjct 61 TNSINFDTSPLSIARASNLEPMDDKLVQDVLLVPVTCGCTGNRSFANISYEINQGDGF 120

Query 124 YFVATTLYQNLTNNHVMNDLNPGLSQFTLPIGIQVVPFLPCKCPSKNQLDGKIYLTIV 183

Sbjct 121 YFVATTSYENLTNNHVMNDLNPVLSPNKLPIGIQVVPFLPCKCPSKNQLDGKIYLTIV 180

Query 184 WKPGDNVSVFVNKLKASPDILSENNYQGNFTAAANLPLVLPVTLPLDIQSPSGDKRKH 243

Sbjct 181 WKPGDNVSVFSDKFGASPEDIMSENNYQGNFTAAANLPLVLPVTLPLDIQSPSGDKRKH 240

Query 244 IGLPVIIGISGCTLLVVSAILLVCCVCLMKMSINRSASAEADKLLSGVSGVSKPT 303

Sbjct 241 IRLPVIIGISGCTLLVLVAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300

Query 304 MYETGAILAETMNLSEQCKIGSEVYKA 330

Sbjct 301 MYETDAIMEATMNLSEQCKIGSEVYKA 327

>dbj|BA085142.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 513 bits (1322), Expect = 2e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVVMFPT-CIEAQSQQTNGTNFSCPSNPSFCCTYTVYISQSPNLFSL 63

Sbjct 1 FPLPLBSQILGLVIMLFSTNIVAQSQDNRTNFCSDSPSPSCCTYTVYIAQSPNLFSL 60

Query 64 TSVSNIFDTSPLSIARASNLEPMDDKLVQDVLLVPVTCGCTGNRSFANISYEINQGDGF 123

Sbjct 61 TNSINFDTSPLSIARASNLEPMDDKLVQDVLLVPVTCGCTGNRSFANISYEINQGDGF 120

Query 124 YFVATTLYQNLTNNHVMNDLNPGLSQFTLPIGIQVVPFLPCKCPSKNQLDGKIYLTIV 183

Sbjct 121 YFVATTSYENLTNNHVMNDLNPVLSPNKLPIGIQVVPFLPCKCPSKNQLDGKIYLTIV 180

Query 184 WKPGDNVSVFVNKLKASPDILSENNYQGNFTAAANLPLVLPVTLPLDIQSPSGDKRKH 243

Sbjct 181 WKPGDNVSVFSDKFGASPEDIMSENNYQGNFTAAANLPLVLPVTLPLDIQSPSGDKRKH 240

Query 244 IGLPVIIGISGCTLLVVSAILLVCCVCLMKMSINRSASAEADKLLSGVSGVSKPT 303

Sbjct 241 IRLPVIIGISGCTLLVLVAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300

Query 304 MYETGAILAETMNLSEQCKIGSEVYKA 330

Sbjct 301 MYETDAIMEATMNLSEQCKIGSEVYKA 327

>dbj|BA085175.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 513 bits (1321), Expect = 3e-143, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVVMFPT-CIEAQSQQTNGTNFSCPSNPSFCCTYTVYISQSPNLFSL 63

Sbjct 1 FPLPLBSQILGLVIMLFSTNIVAQSQDNRTNFCSDSPSPSCCTYTVYIAQSPNLFSL 60

Query 64 TSVSNIFDTSPLSIARASNLEPMDDKLVQDVLLVPVTCGCTGNRSFANISYEINQGDGF 123

Sbjct 61 TNSINFDTSPLSIARASNLEPMDDKLVQDVLLVPVTCGCTGNRSFANISYEINQGDGF 120

Query 124 YFVATTLYQNLTNNHVMNDLNPGLSQFTLPIGIQVVPFLPCKCPSKNQLDGKIYLTIV 183

Sbjct 121 YFVATTSYENLTNNHVMNDLNPVLSPNKLPIGIQVVPFLPCKCPSKNQLDGKIYLTIV 180

Query 184 WKPGDNVSVFVNKLKASPDILSENNYQGNFTAAANLPLVLPVTLPLDIQSPSGDKRKH 243

Sbjct 181 WKPGDNVSVFSDKFGASPEDIMSENNYQGNFTAAANLPLVLPVTLPLDIQSPSGDKRKH 240

Query 244 IGLPVIIGISGCTLLVVSAILLVCCVCLMKMSINRSASAEADKLLSGVSGVSKPT 303

Sbjct 241 IRLPVIIGISGCTLLVLVAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300

Query 304 MYETGAILAETMNLSEQCKIGSEVYKA 330

Sbjct 301 MYETDAIMEATMNLSEQCKIGSEVYKA 327

>dbj|BA085150.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 513 bits (1321), Expect = 3e-143, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVVMFPT-CIEAQSQQTNGTNFSCPSNPSFCCTYTVYISQSPNLFSL 63

Sbjct 1 FPLPLBSQILGLVIMLFSTNIVAQSQDNRTNFCSDSPSPSCCTYTVYIAQSPNLFSL 60

Query 64 TSVSNIFDTSPLSIARASNLEPMDDKLVQDVLLVPVTCGCTGNRSFANISYEINQGDGF 123

Sbjct 61 TNSINFDTSPLSIARASNLEPMDDKLVQDVLLVPVTCGCTGNRSFANISYEINQGDGF 120

Query 124 YFVATTLYQNLTNNHVMNDLNPGLSQFTLPIGIQVVPFLPCKCPSKNQLDGKIYLTIV 183

Sbjct 121 YFVATTSYENLTNNHVMNDLNPVLSPNKLPIGIQVVPFLPCKCPSKNQLDGKIYLTIV 180

Query 184 WKPGDNVSVFVNKLKASPDILSENNYQGNFTAAANLPLVLPVTLPLDIQSPSGDKRKH 243

Sbjct 181 WKPGDNVSVFSDKFGASPEDIMSENNYQGNFTAAANLPLVLPVTLPLDIQSPSGDKRKH 240

Query 244 IGLPVIIGISGCTLLVVSAILLVCCVCLMKMSINRSASAEADKLLSGVSGVSKPT 303

Sbjct 241 IRLPVIIGISGCTLLVLVAVLLVYVYCLMKMTINRSASAEADKLLSGVSGVSKPT 300

Query 304 MYETGAILAETMNLSEQCKIGSEVYKA 330

Sbjct 301 MYET AI+EAATMNLSEQCKIGESVYKA
MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085173.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 513 bits (1320), Expect = 3e-143, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQIIYVVMFF-TCIAAQSQQTNGTNFSCPSNSPPCCTTYVTIISQSPNLFSL 63
F L L +QIL +V+M F T I AQSQ N TNFSCPS+SPPCCTTYVTI+QSPNLFSL
Sbjct 1 FFLPLHSGICLGLVIMLFSTNI VAQSQDQNRNTNFCPSDPSPPCCTTYVTI+AQSPNLFSL 60

Query 64 TSVSNIFDTSPLSIARASNLIQHEEDKILPGQVLLIPVTCGCTGNRSFANISYEINQGSDF 123
T+SNIFDTSPLSIARASNLI+DKL+ QVLL+PVTGCTGNRSFANISYEINQGSDF
Sbjct 61 TNSINIFDTSPLSIARASNLEPMDDKILVKDQVLLIPVTCGCTGNRSFANISYEINQGSDF 120

Query 124 YFVATTLYQNTNWRHVMNDLNPGLSQFTPLIGIQVVPFLCKCPSKNQLDRGIKYLITV 183
YFVATT Y+NTNWR AVMDNP LS LPIGIQVVP FLCKCPSKNQLD+ IKYLITV
Sbjct 121 YFVATTSEYENLTNWRHVMNDLNPVLSNKLPLIGIQVVPFLCKCPSKNQLDRGIKYLITV 180

Query 184 WQPNQNVSVBNKLQASQDILSENNYGNFTAAANLPLVLPVTLPLDIOQSPSGRKRH 243
W+P DNVS VBN+K QASPD+I+SENNYGNFTAA+NLPLVLPVTL L L +SPDGRK
Sbjct 181 WKPDNVSLVBDKQASPEDIMSENNYGNFTAAANLPLVLPVTLPLVARSFSDGRKGG 240

Query 244 IGLPVIIGISGICTLVAVSAILLVWCCLMKSNIRNSASSAETADKLLSGVSGVSKPT 303
I LPVIGISIGTLIV+ A+LLV V CLMK+INRSASSAETADKLLSGVSGVSKPT
Sbjct 241 IRLPVIIGISGICTLVLVLAVLLVYVYCLMKTNIRNSASSAETADKLLSGVSGVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EAATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085157.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 513 bits (1320), Expect = 4e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQIIYVVMFF-TCIAAQSQQTNGTNFSCPSNSPPCCTTYVTIISQSPNLFSL 63
F L L +QIL +V+M F T I AQSQ N TNFSCPS+SPPCCTTYVTI+QSPNLFSL
Sbjct 1 FFLPLHSGICLGLVIMLFSTNI VAQSQDQNRNTNFCPSDPSPPCCTTYVTI+AQSPNLFSL 60

Query 64 TSVSNIFDTSPLSIARASNLIQHEEDKILPGQVLLIPVTCGCTGNRSFANISYEINQGSDF 123
T+SNIFDTSPLSIARASNLI+DKL+ QVLL+PVTGCTGNRSFANISYEINQGSDF
Sbjct 61 TNSINIFDTSPLSIARASNLEPMDDKILVKDQVLLIPVTCGCTGNRSFANISYEINQGSDF 120

Query 124 YFVATTLYQNTNWRHVMNDLNPGLSQFTPLIGIQVVPFLCKCPSKNQLDRGIKYLITV 183
YFVATT Y+NTNWR AVMDNP LS LPIGIQVVP FLCKCPSKNQLD+ IKYLITV
Sbjct 121 YFVATTSEYENLTNWRHVMNDLNPVLSNKLPLIGIQVVPFLCKCPSKNQLDRGIKYLITV 180

Query 184 WQPNQNVSVBNKLQASQDILSENNYGNFTAAANLPLVLPVTLPLDIOQSPSGRKRH 243
W+P DNVS VBN+K QASPD+I+SENNYGNFTAA+NLPLVLPVTL L L +SPDGRK
Sbjct 181 WKPDNVSLVBDKQASPEDIMSENNYGNFTAAANLPLVLPVTLPLVARSFSDGRKGG 240

Query 244 IGLPVIIGISGICTLVAVSAILLVWCCLMKSNIRNSASSAETADKLLSGVSGVSKPT 303
I LPVIGISIGTLIV+ A+LLV V CLMK+INRSASSAETADKLLSGVSGVSKPT
Sbjct 241 IRLPVIIGISGICTLVLVLAVLLVYVYCLMKTNIRNSASSAETADKLLSGVSGVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EAATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085176.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 511 bits (1317), Expect = 8e-143, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQIIYVVMFF-TCIAAQSQQTNGTNFSCPSNSPPCCTTYVTIISQSPNLFSL 63
F L L +QIL +V+M F T I AQSQ N TNFSCPS+SPPCCTTYVTI+QSPNLFSL
Sbjct 1 FFLPLHSGICLGLVIMLFSTNI VAQSQDQNRNTNFCPSDPSPPCCTTYVTI+AQSPNLFSL 60

Query 64 TSVSNIFDTSPLSIARASNLIQHEEDKILPGQVLLIPVTCGCTGNRSFANISYEINQGSDF 123
T+SNIFDTSPLSIARASNLI+DKL+ QVLL+PVTGCTGNRSFANISYEINQGSDF
Sbjct 61 TNSINIFDTSPLSIARASNLEPMDDKILVKDQVLLIPVTCGCTGNRSFANISYEINQGSDF 120

Query 124 YFVATTLYQNTNWRHVMNDLNPGLSQFTPLIGIQVVPFLCKCPSKNQLDRGIKYLITV 183
YFVATT Y+NTNWR AV DNP LS LPIGIQVVP FLCKCPSKNQLD+ IK+LITV
Sbjct 121 YFVATTSEYENLTNWRHVMNDLNPVLSNKLPLIGIQVVPFLCKCPSKNQLDRGIKYLITV 180

Query 184 WQPNQNVSVBNKLQASQDILSENNYGNFTAAANLPLVLPVTLPLDIOQSPSGRKRH 243
W+P DNVS VBN+K QASPD+I+SENNYGNFTAA+NLPLVLPVTL L L +SPDGRK
Sbjct 181 WKPDNVSLVBDKQASPEDIMSENNYGNFTAAANLPLVLPVTLPLVARSFSDGRKGG 240

Query 244 IGLPVIIGISGICTLVAVSAILLVWCCLMKSNIRNSASSAETADKLLSGVSGVSKPT 303
I LPVIGISIGTLIV+ A+LLV V CLMK+INRSASSAETADKLLSGVSGVSKPT
Sbjct 241 IRLPVIIGISGICTLVLVLAVLLVYVYCLMKTNIRNSASSAETADKLLSGVSGVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EAATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085155.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 511 bits (1316), Expect = 1e-142, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQIIYVVMFF-TCIAAQSQQTNGTNFSCPSNSPPCCTTYVTIISQSPNLFSL 63
F L L +QIL +V+M F T I AQSQ N TNFSCPS+SPPCCTTYVTI+QSPNLFSL
Sbjct 1 FFLPLHSGICLGLVIMLFSTNI VAQSQDQNRNTNFCPSDPSPPCCTTYVTI+AQSPNLFSL 60

Query 64 TSVSNIFDTSPLSIARASNLIQHEEDKILPGQVLLIPVTCGCTGNRSFANISYEINQGSDF 123

Sbjct 61 T++SNIFDTSPLSIARASNI+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDGF 120
 T+NSINFDTSPLSIARASNIEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF

Query 124 YFVATTLYQNLTNRHVMNDINPGLSQFTLPIGIQVVPFLCKCPKSNQLDRIKYLITV 183
 YFVATT Y+NLTNH AVMDINP LS LPIGIQV PFLCKCPKSNQLD+ IKYLITV

Sbjct 121 YFVATTSYENLTNRHVMNDINPGLSPNKLPIGQVFPFLCKCPKSNQLDRIKYLITV 180

Query 184 WQPNQNVSVSNKLGASPDILSENNYQNFPTAASNLVPLVPTLLPOLIQSPSDGRKRR 243
 W+P DNVS V+K+ GAS+DI+SENNYQNFPTA+NLPLVLPVT LP L +SPDGRK

Sbjct 181 WKPGDNVSLVSDKFGASPDIMSENNYQNFPTAANNLPVLVPTLLPOLIQSPSDGRKGG 240

Query 244 IGLPVIIGISIGCTLLVVSAILLVCCCLMKMSINRSASAEADKLLSGVSGYVSKPT 303
 I+LPIVIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGYVSKPT

Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVCLMKMLNRSASAEADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET A+EA+TMNLSEQCKIGESVYKA

Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085163.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 511 bits (1315), Expect = 2e-142, Method: Compositional matrix adjust.
 Identities = 265/327 (81%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLAGQILYVVMFF+TCIEAQSQQTNTNFCSPNSPFCETTYVTYIQSPNLFSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFCSPS+SP SCETTY YI+QSPNLFSL

Sbjct 1 FFLPLHSGQLCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPFCETTYVTYIAQSPNLFSL 60

Query 64 TSVSNI+FDTSPLSIARASNI+HEEDKILPGQVLLIPVTGCTGNRSFANISYEINQGDGF 123
 T++SNIFDTSPLSIARASNI+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDGF

Sbjct 61 T+NSINFDTSPLSIARASNIEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120

Query 124 YFVATTLYQNLTNRHVMNDINPGLSQFTLPIGIQVVPFLCKCPKSNQLDRIKYLITV 183
 YFVATT Y+NLTNH AVMDINP LS LPIGIQV PFLCKCPKSNQLD+ IKYLITV

Sbjct 121 YFVATTSYENLTNRHVMNDINPGLSPNKLPIGQVFPFLCKCPKSNQLDRIKYLITV 180

Query 184 WQPNQNVSVSNKLGASPDILSENNYQNFPTAASNLVPLVPTLLPOLIQSPSDGRKRR 243
 W+P DNVS V+K+ GAS+DI+SENNYQNFPTA+NLPLVLPVT LP L +SPDGRK

Sbjct 181 WKPGDNVSLVSDKFGASPDIMSENNYQNFPTAANNLPVLVPTLLPOLIQSPSDGRKGG 240

Query 244 IGLPVIIGISIGCTLLVVSAILLVCCCLMKMSINRSASAEADKLLSGVSGYVSKPT 303
 I+LPIVIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGYVSKPT

Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVCLMKMLNRSASAEADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET A+EA+TMNLSEQCKIGESVYKA

Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085154.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 509 bits (1311), Expect = 4e-142, Method: Compositional matrix adjust.
 Identities = 264/327 (80%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLAGQILYVVMFF+TCIEAQSQQTNTNFCSPNSPFCETTYVTYIQSPNLFSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFCSPS+SPFCETTYVTYI+QSPNLFSL

Sbjct 1 FFLPLHSGQLCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPFCETTYVTYIAQSPNLFSL 60

Query 64 TSVSNI+FDTSPLSIARASNI+HEEDKILPGQVLLIPVTGCTGNRSFANISYEINQGDGF 123
 T++SNIFDTSPLSIARASNI+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDGF

Sbjct 61 T+NSINFDTSPLSIARASNIEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120

Query 124 YFVATTLYQNLTNRHVMNDINPGLSQFTLPIGIQVVPFLCKCPKSNQLDRIKYLITV 183
 YFVATT Y+NLTNH AVMDINP LS LPIGIQV PFLCKCPKSNQLD+ IKYLITV

Sbjct 121 YFVATTSYENLTNRHVMNDINPGLSPNKLPIGQVFPFLCKCPKSNQLDRIKYLITV 180

Query 184 WQPNQNVSVSNKLGASPDILSENNYQNFPTAASNLVPLVPTLLPOLIQSPSDGRKRR 243
 W+P DNVS V+K+ GAS+DI+SENNYQNFPTA+NLPLVLPVT LP L +SPDGRK

Sbjct 181 WKPGDNVSLVSDKFGASPDIMSENNYQNFPTAANNLPVLVPTLLPOLIQSPSDGRKGG 240

Query 244 IGLPVIIGISIGCTLLVVSAILLVCCCLMKMSINRSASAEADKLLSGVSGYVSKPT 303
 I+LPIVIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGYVSKPT

Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVCLMKMLNRSASAEADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET A+EA+TMNLSEQCKIGESVYKA

Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085169.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 507 bits (1305), Expect = 2e-141, Method: Compositional matrix adjust.
 Identities = 264/327 (80%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLAGQILYVVMFF+TCIEAQSQQTNTNFCSPNSPFCETTYVTYIQSPNLFSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFCSPS+SPFCETTYVTYI+QSPNLFSL

Sbjct 1 FFLPLHSGQLCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPFCETTYVTYIAQSPNLFSL 60

Query 64 TSVSNI+FDTSPLSIARASNI+HEEDKILPGQVLLIPVTGCTGNRSFANISYEINQGDGF 123
 T++SNIFDTSPLSIARASNI+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDGF

Sbjct 61 T+NSINFDTSPLSIARASNIEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120

Query 124 YFVATTLYQNLTNRHVMNDINPGLSQFTLPIGIQVVPFLCKCPKSNQLDRIKYLITV 183
 YFVATT Y+NLTNH AVMDINP LS LPIGIQV PFLCKCPKSNQLD+ IKYLITV

Sbjct 121 YFVATTSYENLTNRHVMNDINPGLSPNKLPIGQVFPFLCKCPKSNQLDRIKYLITV 180

Query 184 WQPNQNVSVSNKLGASPDILSENNYQNFPTAASNLVPLVPTLLPOLIQSPSDGRKRR 243
 W+P DNVS V+K+ GAS+DI+SENNYQNFPTA+NLPLVLPVT LP L +SPDGRK

Sbjct 181 WKPGDNVSLVSDKFGASPDIMSENNYQNFPTAANNLPVLVPTLLPOLIQSPSDGRKGG 240

Query 244 IGLPVIIGISIGCTLLVVSAILLVCCCLMKMSINRSASAEADKLLSGVSGYVSKPT 303
 I+LPIVIGISIGCTLLV+V A+LLV V CLMK+INRSASAEADKLLSGVSGYVSKPT

Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVCLMKMLNRSASAEADKLLSGVSGYVSKPT 300

Query 304 MYETGALLKATMNLSEQCCKIGSVYKA 330
 Sbjet 301 MYETDAIMEATMNLSEQCCKIGSVYKA 327

>dbj|BA085166.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 501 bits (1291), Expect = 9e-140, Method: Compositional matrix adjust.
 Identities = 260/324 (80%), Positives = 286/324 (88%), Gaps = 1/324 (0%)

Query 5 FVSLTLGAQLIVYVLMFT-FCIAAQSQQTNTNFCSPNSPPCCETTYVTVYIAQSPNFI 63
 F L L +QIT +V+M F T I AQSQ N ENFCSPNSPPCCETTYVTVYIAQSPNFI 63
 Sbjet 1 FFLPLRLSGLQLCLVIMLESTNIQAQSQQNTNFCSPNSPPCCETTYVTVYIAQSPNFI 60
 Query 64 TVSNIFDTSPLSIARASNLQHEEDKLIPQGVLLIPVTCOCTGNRSFANISYEINQGDGF 123
 T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTCCOCTGNRSFANISYEINQGDGF 123
 Sbjet 61 TNISNLFDTSPLSIARASNLFPMDOKLVKQVLLIPVTCOCTGNRSFANISYEINQGDGF 120
 Query 124 YFVATTLYQNLTNHWAVMDLNPGLSQFTLPIGIQVVPILFCCKPSKNGLDGRGIYLTITV 183
 YFVATY +GNTNHWAVMDLN L L LPIQIQV PFLCKCKPSKNGLD+ IYLTITV 183
 Sbjet 121 YFVATTYENITNHWAVMDLNPVLSNKLPIGQVVPILFCCKPSKNGLDKEIRLYITV 180
 Query 184 WKQPNVSVFVSNKLGASPDILSENNYQNTAASNLVPLVPTLLPDLIQSPDGRKRR 243
 W+P DNVS V8+K GAS+DI+SENNYQNTAA+NLVPLVPT L L +SPDGRK 243
 Sbjet 181 WKQPNVSVLVBKFGASPEDIMSENNYQNTAANNLPLVPTLLPDLVPLARSPDGRKGG 240
 Query 244 IGLPVLIGISGLTLLVVSAILLVCCCLMKMSINRSASAEADTKLLSGVSGYVSKPT 303
 I LPLVIGISGLTLLV+ A+LLV V CLMK+INRSASAE ADTKLLSGVSGYVSKPT 303
 Sbjet 241 IGLPVLIGISGLTLLVLLVLAWLIVYVYCKMKTINRSASAEADTKLLSGVSGYVSKPT 300
 Query 304 MYETGALLKATMNLSEQCCKIGSV 327
 MYET A+EA+MNLSEQCCKIG SV 327
 Sbjet 301 MYETDAIMEATMNLSEQCCKIGSV 324

>emb|CA002936.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=349

Score = 482 bits (1240), Expect = 8e-134, Method: Compositional matrix adjust.
 Identities = 238/351 (67%), Positives = 288/351 (82%), Gaps = 4/351 (1%)

Query 53 YIQSQPNFLISLTVSNIFDTSPLSIARASNLQHEEDKLIPQGVLLIPVTCOCTGNRSFAN 112
 Y +QSQPNFLISL++S+IF+ SPL IA+ASN+ E+ KLIP Q+LL+PVTCCOCT N SFAN 112
 Sbjet 1 YRAQSQPNFLISLNSIDIFNLSPFLRIAKASNLAEADKLLPDQLLLVPTVTCOCTGNRSFAN 60
 Query 113 ISYEINQGDGFYFVATTLYQNLTNHWAVMDLNPGLSQFTLPIGIQVVPILFCCKPSKNGLD 172
 I+V I QGD+T++ T YQNLTN+ + NP L S L P+ +V PFLCKCKPSKNGLD 172
 Sbjet 61 TYSYQNTNFIISYQNTNFIISYQNTNFIISYQNTNFIISYQNTNFIISYQNTNFIISYQNTNFI 120
 Query 173 DRGKILYITVWQPNVSVFVSNKLGASPDILSENNYQNTAASNLVPLVPTLLPDL 232
 T+GKILYITVWQPNVSVFVSNKLGAS +L+ENN+ NFTA+N VLIPT L L 232
 Sbjet 121 NKGKILYITVWQNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSLVPTLLPDL 178
 Query 233 IQSPDGRKHRI-GLPVLIGISGLTLLVVSAILLVCCCLMKMSINRSASAEADTKLL 291
 Q S+GRK L +IIGISGL +V+ +IV V CLMK LNRS SS+ETADKL 291
 Sbjet 179 DQPSNGRKRSSQNLALLIGISGLSAFFLIVTLISLVVYVCLMKLNRSSTSSSETADKL 238
 Query 292 ISGVSGYVSKPTMYETGALLKATMNLSEQCCKIGSVYKANIEGRVLAVKRFKEDVTEELK 351
 ISGVSGYVSKPTMYE A+H TMLNLS+ CKIGSVYKANIE+GVAVK R+D +EELK 351
 Sbjet 239 ISGVSGYVSKPTMYEIDAEMGTMLNLSCKIGSVYKANIDGRVLAVKRIKDKASEL 298
 Query 352 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLSEWLFS+SKTSNS 402
 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLSEWLFS+SKTSNS 402
 Sbjet 299 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLSEWLFS+SKTSNS 348

>emb|CA002948.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=337

Score = 465 bits (1197), Expect = 7e-129, Method: Compositional matrix adjust.
 Identities = 228/339 (67%), Positives = 275/339 (81%), Gaps = 3/339 (0%)

Query 48 ETYVTVISQSPNFIISLTVSNIFDTSPLSIARASNLQHEEDKLIPQGVLLIPVTCOCTGN 107
 ETYV Y +QSPNFIISL++S+IF+ SPL IA+ASN+ E+ KLIP Q+LL+PVTCCOCT N 107
 Sbjet 1 ETYVAYRAQSPNFIISLNSIDIFNLSPFLRIAKASNLAEADKLLPDQLLLVPTVTCOCTGN 60
 Query 108 HSFANISYEINQGDGFYFVATTLYQNLTNHWAVMDLNPGLSQFTLPIGIQVVPILFCCKP 167
 SFANISYEINQGDGFYFVATTLYQNLTNHWAVMDLNPGLSQFTLPIGIQVVPILFCCKP 167
 Sbjet 61 HSFANISYEINQGDGFYFVATTLYQNLTNHWAVMDLNPGLSQFTLPILDTVSVPLFCCKP 120
 Query 168 SKNQLDRGKILYITVWQPNVSVFVSNKLGASPDILSENNYQNTAASNLVPLVPT 227
 SKNQL++GKILYITVWQNDNV+ V8+K GAS +L+ENN+ NFTA+N VLIPT 227
 Sbjet 121 SKNQLNKGKILYITVWQNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSLVPT 178
 Query 228 LPLDILQSPDGRKHRI-GLPVLIGISGLTLLVVSAILLVCCCLMKMSINRSASAE 286
 L P L Q S+GRK L +IIGISGL +V+ +IV V CLMK LNRS SS+E 286
 Sbjet 179 LPLDILQSPDGRKRSSQNLALLIGISGLSAFFLIVTLISLVVYVCLMKLNRSSTSSSE 238
 Query 287 TADKLLSGVSGYVSKPTMYETGALLKATMNLSEQCCKIGSVYKANIEGRVLAVKRFKEDV 346
 TADKLLSGVSGYVSKPTMYE A+H T NLS+ CKIGSVYKANIE+GVAVK R+D 346
 Sbjet 239 TADKLLSGVSGYVSKPTMYEIDAEMGTMLNLSCKIGSVYKANIDGRVLAVKRIKDKA 298
 Query 347 TEELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENG 385
 +EELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENG 385
 Sbjet 299 SEELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENG 337

>emb|CA002942.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=334

Score = 462 bits (1190), Expect = 4e-128, Method: Compositional matrix adjust.
 Identities = 227/336 (67%), Positives = 274/336 (81%), Gaps = 3/336 (0%)

Query 53 YIQSQPNFLISLTVSNIFDTSPLSIARASNLQHEEDKLIPQGVLLIPVTCOCTGNRSFAN 112

Subject	1	YRQSPGSDLSIGTSDINPILSPILSKAASNTIEADKKLLPQDILLVPVCTCKTKNSHPAN	60
Query	1	ISVEYNGDQSVFYVATYLLQNTNHRVAWDNLGDSQDILQVQVPLFCCKSPKSN	172
Subject	61	ITYSYIGQD+P+T+T YONITM+ + NP LS LP+ + +P+LFCCKSPKSNQJ	120
Query	1	DIGIKYLLVQDNDVNVFSPKSGASPDQILSENNNGYNTAASNLPLVPLITPL	232
Subject	121	+GKLYLL+VWD NDNV+ VSK+GAS+ +L+ENN+ NPTA+ +L+LPLV LPL L	176
Subject	233	QSGDILVQDNDVNVFSPKSGASPDQILSENNNGYNTAASNLPLVPLITPL	232
Subject	293	QSGDILVQDNDVNVFSPKSGASPDQILSENNNGYNTAASNLPLVPLITPL	232
Subject	1	QPSNQRKRRKT+GLVLTITSLGSLT+LVVYSALLVCCVCKKKKASRASSAETADKL	291
Subject	179	QPSNQRKRRKT+GLVLTITSLGSLT+LVVYSALLVCCVCKKKKASRASSAETADKL	291
Subject	192	ISGVSGVSKPMTYETGAILEATMGNTISNCKCTKGSVYKANIGKVLVAKRFKEETWELK	334
Subject	239	ISGVSGVSKPMTYETGAILEATMGNTISNCKCTKGSVYKANIGKVLVAKRFKEETWELK	334
Subject	352	ILQKVNENLVKLVMGVSSNDGNCFFVYETAEKSL 387	
Subject	394	ILQKVNENLVKLVMGVSSNDGNCFFVYETAEKSL 387	
Subject	394	ILQKVNENLVKLVMGVSSNDGNCFFVYETAEKSL 387	

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>emb|CA002960.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
var. truncatula]
length=333
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Score = 458 bits (1179), Expect = 9e-127, Method: Compositional matrix adjust.
Identities = 225/335 (67%), Positives = 272/335 (81%), Gaps = 3/335 (0%)

Query	53	YQSPNFSLISLTSVSNIDPITSLPLSTARSINQHEEDKLLPQGVILLPCTGCCTGCFN	112
Sbjct	1	YQSPNFSLISLTSVSI++S+I+ SPL LIAASR++ +E KLIP +L+P+PVTGCSTN SFAN YRQSPNFSLISLTSNDISLITSLPLSTARSINDEAKDLIPQGVLPVCTGCCTGKHSFN	160
Query	113	TSVEINGDQSVYFVATYILQNLNHAAVNDINGLSGLSTPTLIGIIVGWIPLECKSPKQOL	72
Sbjct	61	++T GDG++ ++ T YQNLN++ ++ ND LS LPT ++ +P+LECKSPKQOL TVYSRGAGCTF++TSLTSGVSN++EFKNN++NLSTLPTLIGIIVGWIPVLECKSPKQOL	120
Query	173	DGKIGYLLTWGQNDVYFVBNKLGASQDILSESNYNGNCTAASNVLPIVPTVLLD	232
Sbjct	121	NKIGYLLTWGQNDVYFVBNKLGASQDILSESNYNGNCTAASNVLPIVPTVLLD NKIGYLLTWGQNDVYFVBNKLGASQVEMIAHNN--NPTASNRVSLPIVPTVLEKL	236
Query	233	TPQSPDQDKRHRT-GLVPTIGLHGLCTLLVJVSVALCLMKMLGRASASATADKL	291
Sbjct	173	Q+GRK L+IIIGSLG ++V +LV CVCKM LMR5 S+BSATADKL TPQSPNGKRSSSNGLHGLIGSLGSAFTLVLTLSLVYGLVLMKMLRSTTSSTADKL	338
Query	292	LSGVSQSVSKPMTYETAGLEATLNNLEOQKIGESVYANKIVGLAKVRFKEVTEELK	351
Sbjct	239	LSGVSQSVSKPMTY A++E T NLS+ CRIGESVYANKIVGL++VLAU+K+D +EELK LSGVSQSVSKPMTYEDAGLEATLNNLSDNCKIGESVYANKIDGVLVAKIKKDESLK	398
Query	352	TLQKNVGNLKLVMQVSSNDGNCVFPYEAENG	386
Sbjct	293	TLQKNVGNLKLVMQVSSNDGNC+P+VEYEAENG	333

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>gb|AA019130.1|AC103891.10 Putative protein kinase [Oryza sativa Japonica Group]
gb|AB794815.1| Protein kinase domain containing protein [Oryza sativa (Japonica
cultivar-group)]
gb|EA226175.1| hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]
length=624
```

Score = 426 bits (1095), Expect = 5e-117, Method: Compositional matrix adjust.
Identities = 249/598 (41%), Positives = 357/598 (59%), Gaps = 45/598 (7%)

Query 11 GAQILYVLMF-FTCIEAQSQT-NGINFSCPSNSPPSCETYVTYISQSPNFLSLTSVSN 68
G IL VV+ F EA + T F+C ++P C+T+V Y +QSP FL L ++S+

Query	69	IFTDPTSGTAAASNLHQHDEKILQVQVLLIPVTCGTSFASNSFANISYEINDEDSYFVAT	128
Subject	63	+VS I A + L +E +LPG GL Y FVG CGTG RSFAN +I D+P +A LFGVSRALASANKLITDGVLLPGVLLIPVKGCGTARSFANVPIPRRDTFFGLAV	122
Query	123	TLVQNLNVAENANINPGLSQPTLPIGIVQVLEFLRCKPSKQDLGKLYLTHVWMD	128
Subject	123	+AFENLIDFVLEINLPAAATLEPNAFVWFLPFCRCPTRFELSASRLIVYVWMDG	122
Query	189	VSNSVKNGLASQDPLLEISNCTPAAANLNLVITLPLD-----IQSPSDGR	141
Subject	183	+VS VS + AS +I + N N T A+ P KLV+P P I + DVSVMASALNAAANAAASNGVAGNSTQTQGVLLFVSPGVPRFLPYTGAIADPGAK	242
Query	242	HRGILVPIIGISIGLSTAGLVAITLLVLCVCK-----KINSRASA	283
Subject	243	+S + RGR--IIVATISAGLGF--VACAVITCALIYARVYRKAVPKRVHSKPLSWTSKLNRFDS	293
Query	284	SAGTA-----DKLLSGVSQVSPYMYTGAILEATNLSBQCKISGEVYKANTIKYVL	337
Subject	299	+A +A DKLL+ VS + + PP + + +EATNML RQCK+Q S Y A+NE +V NSISARINMGOKLILVSGYDKRPIIFREEIEATNMLDQCKLGSSTYRANLEWF	358
Query	339	AVAKRKEDVLETKILQVKNHNLNGLVMSVSSNDG-CFVYVEYSNLSLEAFKAC	394
Subject	339	AVAKPKNVAGELMRVLRNHNHNLKLAGISITGADGVAFYVSEKSGKGLKYLQKPP	394
Query	397	SETSNKR--TSLTMCQRTISAVMSVGLQMYLMEHAYFVRHIRTDSKSLNDSFKAKA	454
Subject	419	+S +L+R CR +IAD+V GL Y+EH P +VH DI + NILL + FAK+ CSQSSSVAT+SGDRGR+LGLLXLLHSGHSGVQVGLVGLVGLGAFK+K	478
Query	455	NPSNKR--FTTNMNSKIDVAFVRLNGLKRAKMTTTEGEVWMLWKRPQLE	511
Subject	479	+NFSI-A + DVFAG+ +ELL+GR+A B +M +M NPSLAKAPAAVDAASSTDSVAFGLLILGLSGR+AVARGVIGLIMRTLEITDVG	538
Query	512	ENRERELKRWMDPKLNYLIVLISASLAVNCTASLSRPTIAIVLISLITSL	569
Subject	512	+R +LRKMDK L Y +D +ALSA +A CR +R +R +EY +SLSL+Q ENRERELKRWMDPKLNYLIVLISASLAVNCTASLSRPTIAIVLISLITSL	596

>ref|XP_002468236.1| hypothetical protein SORBIDRAFT 01g042230 [Sorghum bicolor]

gb|EER95234.1| **G** hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]
Length=631

GENE ID: 8085264 SORBIDRAFT_01g042230 | hypothetical protein [Sorghum bicolor]
(10 or fewer PubMed links)

Score = 426 bits (1034), Expect = 5e-117, Method: Compositional matrix adjust.
Identities = 243/592 (41%), Positives = 350/592 (59%), Gaps = 56/592 (9%)

Query 28 QSQQTNGTGFSCP-----SNSPSCCTVYVYISQSPNLSLTSVNSIFDTSPSLIARA 80
Sbjct 18 QAGQDNTLYVTPAQFACNVSSSPPCDCTVYVYRTQSPGYDGLSISDLFTGSOARLASA 77

Query 81 SNLQHEERDLIPQGVLLIPVT-QCGTGNRSFANISYEINQDGSFYVATTLYQNLNWHIA 139
+ L E+ L PQQ LL+PV+ CCGTQ SFAN+Y I QGD+ +A Y+NLT +
Sbjct 78 NGLSSDGVLPQGVLLIPVPCGCTGGWFSANVYPIRQGDFTFNLARVSTNLTLYQL 137

Query 140 VNLINPGLSQFTLPDIPGIVQVITPLFCCKPCPKNLDGRIKILYTHVQPMNDVNSVKNLGA 199
+ +ND T+ + I2 V+ PLFC+CP+ I+TVWQ D +B VS +
Sbjct 138 IQNLNFRSPVPSLQGVQGVVTPFLFCRCPCAPAEARS-----FITVWQADTMSQVSKLMT 193

Query 200 SPQDILSENNYQNTFAAS-NLPVLIPVTPLLPD-----IQSPDGRKIRIGLPIVIGI 252
+ + I+ NN + +AS P+LIPV P L S DG+ VIIG
Sbjct 194 TEDEIAEANNVSSASASLVGQPMILPVQORPALPLPHYAASAGDGKSWRRRAVILGA 253

Query 253 SLGCTLLVVVSAILLVCCVCL-----MKSLNRSASAE----- 286
S+ + VV A L V + L+ M+ +R A + +
Sbjct 254 SVSOS--VVALAAFLVAILARXKPKPMRLSRFVNKLTWSRNFQHDSSNSFAHM 311

Query 287 ---TADKLLSGVSGVSKPMYTGAILATMNLSECKIGESVYKANIQGVLAVERFK 343
+ +L+ QV+ + K+ + I+ATMNL ECKIG + Y+A + +G+V AVK K
Sbjct 312 MKLGGKLLTGVSFEIDKPIIFLEEIMEATMNLDERCKIGSTYTRAKLQGVFAVPAK 371

Query 344 EDVTEELKIQVNRHGNLVLKMGVSSNDGN-CFVVVEYAENGSEELWFAKSCSETS 402
DV+ ELK+Q VNR NL+KL G+S DG+ P+VVE+AE GSL+WL+ K S + S
Sbjct 372 GUVSAELKMMQVNRHNLKLAGISIGTDGYAFVVEFAEKGLDKMLYKQPPSALPS 431

Query 403 R---TSLTWCQRISIAVDSMGLQYMEHAYPRVIRDRITSSNILLDSNFKAIANFMS 458
+L+M QR+SLA+DV+ GL YMEH P +VH DI + NLL + +G R+I + FB+
Sbjct 432 SCCTVATLAWGLSLALVWGLYMEHTQPSMVHGDIDARNLLIABAFKLSQFSL 491

Query 459 AR-TFTNPMNSKIDVFARGVLLIELLTGRKAMTKENGSEVVMWKDIFQDQENREER 517
A+ + DVFAFG+L+ELL+GR+AM + R+ ML+I+ + D + RE +
Sbjct 492 AKPATADAAATSSDVFAFGLLLELLSGRAVEARVGEICMLWREIRGLVDAGDKREAK 551

Query 518 LKRWMDPKLNYYPIDVALSASLAVNCTAKSLSRPTIAEIVLSLSLTP 569
L KRWMD P L + Y + D ALSA +A CT D + RP +E+V SLS+L QP
Sbjct 552 LGRWMDPLGSEYRMDALSIAGMARACTEEDARREANMTVEVLSLVLPQ 603

gb|EAX89155.1| hypothetical protein OsI_10648 [Oryza sativa Indica Group]
Length=624

Score = 424 bits (1090), Expect = 2e-116, Method: Compositional matrix adjust.
Identities = 248/598 (41%), Positives = 357/598 (59%), Gaps = 45/598 (7%)

Query 11 GAQILVYVIMF-FTCIAESQQT-NGTNFSCPSNPPSCCTVYVYISQSPNLSLTSVSN 68
G IL VV+ P +A + T P+C + +P C+ +V Y +QSP FL L + +B+
Sbjct 5 GLCILAIVAFIQLAGGAVATDARARRACNVASAP--CDTFVYRTQSPGFGLDGLNSID 62

Query 69 IPTDPSLISARASNLQHEEDKLPQGVLLIPVTGCGTGNRSFANISYEINQDGSFYVAT 128
+ F S I+ A A+ L E+ L+PQQ LL+PV CCGTQ RSFAN+Y I+ D+P+ +A
Sbjct 63 LFGQSRALIASANKLITTEDGVLPQGVLLIPVPCGCTGNRSFANVYPIRQPDTPGLAV 122

Query 129 TLQNLNWHIAVMDINPGLSQFTLPDIPGIVQVITPLFCCKPCPKNLDGRIKILYTHVQPMND 188
+ +NLT+ + V +LNP L +VV+PLFC+CP+ +L G L +L+TVWQ D 188
Sbjct 123 TAFENLTFDEVLNPAEATRLPQWQEVVPLFCRCPTRELSAGSRLTVYVWQPD 182

Query 189 NVSPVSKLGASPDQILSENNYQNTFAASNLVLPVTPLLPD-----IQSPDGRK 241
+VS VS + AS +I + N N T A+ PVLIPV+ P I+ + K
Sbjct 183 DVSVVSAIMNAAASNTAASNGVAGNSTFAQGVLLIPVQSPFPPFLTYGAIALDPAQAG 242

Query 242 HRGTLFVIGISLQCTLLVVSAILLVCCVCL-----MKSLNRSAS 283
R R G +P+ S+ +V Y+ + + + KSLNR S
Sbjct 243 HRHG---IIVATSISAGSF--VACAVLCTAILAYRRYKKAQVFKHSPKLSWTSKLNRFDS 298

Query 284 SAETA-----DKLLSGVSGVSKPMYTGAILATMNLSECKIGESVYKANIQGVLA 397
+ + A DKLL+ VS + + KP + + I+ATMNL ECK+G S Y+AN+E +V
Sbjct 299 NSIARMINGDGLKLSVQFIDKPIIFREEIMEATMNLDECKLGSSYFRANLEREV 358

Query 338 AVKRPKEDVTEELKIQVNRHGNLVLKMGVSSNDGN-CFVVVEYAENGSEELWFAKSC 416
AVK R +V EL+ +Q VNR NL KL G+S DG+ P+VVE+AE GSL+WL+ K R
Sbjct 359 AVKRAKRNVAQELKMMQVNRHNLKLAGISIGTDGYAFVVEFAEKGLDKMLYKQPP 491

Query 397 SETSNR--TSLTWCQRISIAVDSMGLQYMEHAYPRVIRDRITSSNILLDSNFKAKIA 454
+S +L+M QR+SLA+DV+ GL Y+HEH P +VH D+ + NLL + F+A+ +
Sbjct 419 CSQPSSSSVATLSMDQLGIALDVGALLYLBHTQPSMVHGDIDARNLLIABTAGFRALKS 478

Query 455 NFMSAR---TFTNPMNSKIDVFARGVLLIELLTGRKAMTKENGSEVVMWKDIFQDQEN 511
NFS+A+ + + DVFAFG+L+ELL+GR+A+ + E+ ML +I+ + D
Sbjct 479 NFSLAKPAATVDAATSSDVFAFGLLLELLSGRAVEARVGEIGMLWREIRTVLVDAGG 538

Query 512 ENREERLRKRWMDPKLNYYPIDVALSASLAVNCTAKSLSRPTIAEIVLSLSLTP 569
R + +L+NDP N Y +D ALSA +A CT D + RP +AEI SLS+L QP
Sbjct 539 DRAKRLRWMDPLGSEYRMDALSIAGMARACTEEDARREANMTVEVLSLVLPQ 596

>emb|CAO02953.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=313

Score = 417 bits (1071), Expect = 3e-114, Method: Compositional matrix adjust.
Identities = 206/315 (65%), Positives = 253/315 (80%), Gaps = 3/315 (0%)

Query 53 YIQSPNFSLSLTSVNSIFDTSPSLIARA-----SNSPSCCTVYVYISQSPNLSLTSVSN 112
Y +QSPNFSLSLTSVNSIFDTSPSLIARA-----SNSPSCCTVYVYISQSPNLSLTSVSN
Sbjct 1 YRAQSPNFSLSLTSVNSIFDTSPSLIARA-----SNSPSCCTVYVYISQSPNLSLTSVSN 60

Query 113 ISVEINQDGSFYFVATTLYQNLTNWHAVMDINPGLSQFTLPIGIQVVPFLPCKCPKSNQ 172
 +I+Y I GQD+P+ ++ T YQNLTN+ + NP LS LP+ +V +PLPCKCPKSNQ 172
 Sbjct 61 TYSIKQDNFPLISTGYQNTNLYLEFKNFNMPLSPTLLPDTKYVSPFLPCKCPKSNQ 120

Query 173 DRGKYLITHVWQDNPNVSVFVNKLQASQDILSENNYQGNFTAAASNLPVLIPVTLPEL 232
 +GIRYLIIT+VWQ DNNV+ VSK GAS +L+ENN+ NPTA+H VLIPTV LP L 232
 Sbjct 121 NKGIRYLITYVWQDNVDNVLVSSKFGASQVEMLAENNH--NFTASTNRSLVLPVTSLEPL 178

Query 233 IQSPSDGRKHRI-GLPVIITIGISLGTCLLVVVSAILLVVCCLMKKSLNRSASSAETADKL 291
 Q S+GRK L +IIGISIG ++V + IV V CLMK LNRS SS+ETADKL 291
 Sbjct 179 DQPSNNGRASSQNLALLIGISLGSAAFLVLVLTLSLVVYVCLMKKRLNRSTSSAETADKL 238

Query 292 ISGVSGYVSKFPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 +GVSGYVSKFPMYE AIE T MNLSE+ CKIGESVYKANI+GV+LAVK+ K+D +EELK 351
 Sbjct 239 ISGVSGYVSKFPMYETDAIMEGTNLSGONCKIGESVYKANIDGRVLAVKRIKKAASELK 298

Query 352 ILQKVNHNKLVKLM 366
 ILQKVNHNKLVKLM
 Sbjct 299 ILQKVNHNKLVKLM 313

>emb|CAO02964.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 emb|CAO02968.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=313

Score = 414 bits (1065), Expect = 1e-113, Method: Compositional matrix adjust.
 Identities = 253/313 (80%), Positives = 251/313 (80%), Gaps = 3/313 (0%)

Query 53 YISQSPNPLISITSVSNIFDTPSLIARASNLQHEEDKLIPQGVLLIPVTCGCTGNRSFAN 112
 Y +QSPNPLISL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGCT N SFAN 112
 Sbjct 1 YRAQSPNPLISLNSIDIFNLSPRLAKASNIEADKKLPDQLLLVPTVTCGCTGNRSFAN 60

Query 113 ISVEINQDGSFYFVATTLYQNLTNWHAVMDINPGLSQFTLPIGIQVVPFLPCKCPKSNQ 172
 +I+Y I GQD+P+ ++ T YQNLTN+ + NP LS LP+ +V +PLPCKCPKSNQ 172
 Sbjct 61 TYSIKQDNFPLISTGYQNTNLYLEFKNFNMPLSPTLLPDTKYVSPFLPCKCPKSNQ 120

Query 173 DRGKYLITHVWQDNPNVSVFVNKLQASQDILSENNYQGNFTAAASNLPVLIPVTLPEL 232
 +GIRYLIIT+VWQ DNNV+ VSK GAS +L+ENN+ NPTA+H VLIPTV LP L 232
 Sbjct 121 NKGIRYLITYVWQDNVDNVLVSSKFGASQVEMLAENNH--NFTASTNRSLVLPVTSLEPL 178

Query 233 IQSPSDGRKHRI-GLPVIITIGISLGTCLLVVVSAILLVVCCLMKKSLNRSASSAETADKL 291
 Q S+GRK L +IIGISIG ++V + IV V CLMK LNRS SS+ETADKL 291
 Sbjct 179 DQPSNNGRASSQNLALLIGISLGSAAFLVLVLTLSLVVYVCLMKKRLNRSTSSAETADKL 238

Query 292 ISGVSGYVSKFPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 +GVSGYVSKFPMYE AIE T MNLSE+ CKIGESVYKANI+GV+LAVK+ K+D +EELK 351
 Sbjct 239 ISGVSGYVSKFPMYETDAIMEGTNLSGONCKIGESVYKANIDGRVLAVKRIKKAASELK 298

Query 352 ILQKVNHNKLVKLM 366
 ILQKVNHNKLVKLM
 Sbjct 299 ILQKVNHNKLVKLM 311

>emb|CAO02944.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=307

Score = 408 bits (1049), Expect = 1e-111, Method: Compositional matrix adjust.
 Identities = 201/309 (65%), Positives = 247/309 (79%), Gaps = 3/309 (0%)

Query 53 YISQSPNPLISITSVSNIFDTPSLIARASNLQHEEDKLIPQGVLLIPVTCGCTGNRSFAN 112
 Y +QSPNPLISL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGCT N SFAN 112
 Sbjct 1 YRAQSPNPLISLNSIDIFNLSPRLAKASNIEADKKLPDQLLLVPTVTCGCTGNRSFAN 60

Query 113 ISVEINQDGSFYFVATTLYQNLTNWHAVMDINPGLSQFTLPIGIQVVPFLPCKCPKSNQ 172
 +I+Y I GQD+P+ ++ T YQNLTN+ + NP LS LP+ +V +PLPCKCPKSNQ 172
 Sbjct 61 TYSIKQDNFPLISTGYQNTNLYLEFKNFNMPLSPTLLPDTKYVSPFLPCKCPKSNQ 120

Query 173 DRGKYLITHVWQDNPNVSVFVNKLQASQDILSENNYQGNFTAAASNLPVLIPVTLPEL 232
 +GIRYLIIT+VWQ DNNV+ VSK GAS +L+ENN+ NPTA+H VLIPTV LP L 232
 Sbjct 121 NKGIRYLITYVWQDNVDNVLVSSKFGASQVEMLAENNH--NFTASTNRSLVLPVTSLEPL 178

Query 233 IQSPSDGRKHRI-GLPVIITIGISLGTCLLVVVSAILLVVCCLMKKSLNRSASSAETADKL 291
 Q S+GRK L +IIGISIG ++V + IV V CLMK LNRS SS+ETADKL 291
 Sbjct 179 DQPSNNGRASSQNLALLIGISLGSAAFLVLVLTLSLVVYVCLMKKRLNRSTSSAETADKL 238

Query 292 ISGVSGYVSKFPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 +GVSGYVSKFPMYE AIE T MNLSE+ CKIGESVYKANI+GV+LAVK+ K+D +EELK 351
 Sbjct 239 ISGVSGYVSKFPMYETDAIMEGTNLSGONCKIGESVYKANIDGRVLAVKRIKKAASELK 298

Query 352 ILQKVNHN 360
 ILQKVNHN
 Sbjct 299 ILQKVNHN 307

>emb|CAO02946.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=305

Score = 404 bits (1037), Expect = 2e-110, Method: Compositional matrix adjust.
 Identities = 199/307 (64%), Positives = 245/307 (79%), Gaps = 3/307 (0%)

Query 53 YISQSPNPLISITSVSNIFDTPSLIARASNLQHEEDKLIPQGVLLIPVTCGCTGNRSFAN 112
 Y +QSPNPLISL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGCT N SFAN 112
 Sbjct 1 YRAQSPNPLISLNSIDIFNLSPRLAKASNIEADKKLPDQLLLVPTVTCGCTGNRSFAN 60

Query 113 ISVEINQDGSFYFVATTLYQNLTNWHAVMDINPGLSQFTLPIGIQVVPFLPCKCPKSNQ 172
 +I+Y I GQD+P+ ++ T YQNLTN+ + NP LS LP+ +V +PLPCKCPKSNQ 172
 Sbjct 61 TYSIKQDNFPLISTGYQNTNLYLEFKNFNMPLSPTLLPDTKYVSPFLPCKCPKSNQ 120

Query 173 DRGKYLITHVWQDNPNVSVFVNKLQASQDILSENNYQGNFTAAASNLPVLIPVTLPEL 232
 +GIRYLIIT+VWQ DNNV+ VSK GAS +L+ENN+ NPTA+H VLIPTV LP L 232
 Sbjct 121 NKGIRYLITYVWQDNVDNVLVSSKFGASQVEMLAENNH--NFTASTNRSLVLPVTSLEPL 178

Query 233 IQSPSDGRKHRI-GLPVIITIGISLGTCLLVVVSAILLVVCCLMKKSLNRSASSAETADKL 291

Sbjct 179 Q S+GRK L +IIIGISLG ++V + LV V CLMKM LNRS SS+ETADKL 238
 DQPSNGRGRSSSQNLALIGISLGSFAFVLVLTLSIVVYVCLMKMRINRSTSSSETADKL
 Query 292 LSGVSGYVSKPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 LSGVSGYVSKPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK
 Sbjct 239 LSGVSGYVSKPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 298
 LSGVSGYVSKPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK
 Query 352 ILQKVN 358
 ILQKVN
 Sbjct 299 ILQKVN 305
 ILQKVN

>emb|CA002962.1| IyM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=304

Score = 400 bits (1028), Expect = 3e-109, Method: Compositional matrix adjust.
 Identities = 198/306 (64%), Positives = 244/306 (79%), Gaps = 3/306 (1%)

Query 53 YISGPNFSLISLTVSNIDTSPSLTARASNLQHEEDKLIPGQVLLIPVTCGGCTKMRNSAF 112
 Y GSPNFSLSLTVSNIDTSPSLTARASNLQHEEDKLIPGQVLLIPVTCGGCTKMRNSAF
 Sbjct 1 YRAQSPNFSLSLTVSNIDTSPSLTARASNLQHEEDKLIPGQVLLIPVTCGGCTKMRNSAF 60
 Query 113 ISYEINQGDSPFYVATTIYQNLTNHVAAMDINPGLSQFTLPIGIQVPIPLCKCPKSNQ 172
 I+Y I QGD+P++ T YQNLTN+ + NP LS LP+ +V +PLCKCPKSNQ
 Sbjct 61 ITYSIQGDNFILSITSYQNLINYLEFKNFNPMLPTLLPLDTKVSVPFLCKCPKSNQ 120
 Query 173 DAGIKYLITVWQPNNDVSPVSNKLGASPDILSENNOYNTAASNLVPLVPTLLDPL 232
 +DGKYLITVWQPNNDVSPVSNKLGASPDILSENNOYNTAASNLVPLVPTLLDPL
 Sbjct 121 +DGKYLITVWQPNNDVSPVSNKLGASPDILSENNOYNTAASNLVPLVPTLLDPL 178
 Query 233 IQSPSGRKHRI+GLVPIIGISLQCTLLVIVVAILVCCCKMKKSNR+AGASGATADKL 291
 Q S+GRK L +IIIGISLG ++V + LV V CLMKM LNRS SS+ETADKL
 Sbjct 179 DQPSNGRGRSSSQNLALIGISLGSFAFVLVLTLSIVVYVCLMKMRINRSTSSSETADKL 238
 Query 292 LSGVSGYVSKPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 LSGVSGYVSKPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK
 Sbjct 239 LSGVSGYVSKPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 298
 LSGVSGYVSKPMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK
 Query 352 ILQKVN 357
 ILQKVN
 Sbjct 299 ILQKVN 304
 ILQKVN

>ref|XP_002517029.1| G serine-threonine protein kinase, plant-type, putative [Ricinus communis]

gb|EF45192.1| G serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 Length=615

GENE ID: 8280185 RCOM_090940 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 356 bits (913), Expect = 6e-96, Method: Compositional matrix adjust.
 Identities = 221/584 (37%), Positives = 321/584 (54%), Gaps = 2/584 (12%)

Query 32 TNGTIFPCSPSPSPSCPTVTVYISQSPNFIPLSTVSNIDTSPSLTARASNLQHEEDKL 91
 T+G S S +V +ENEL L SV++G S L+ S N+ L I
 Sbjct 30 TDGITCTVNCN+SNP-CQYAFYRAMAFNFDLISAGVDLFSVRIMISEPENISPPSPSLI 88
 Query 92 PQGVLLIPVTCGGCTKMRNSAFIYQNLTNHVAAMDINPGLSQFTLPIGIQVPIPLCKCPKSNQ 206
 P Q L +P+G C T N N+AN+SY I +D+FY V+T+QNT+ AV +NP
 Sbjct 89 PQNSLFPVISCSCRAINSTNLN+ANLSYTIKDDTFLVSTTQFQNLITTYQAVQVNNET 148
 Query 147 LSGFTLPIGIQVPIPLCKCPKSNQDREGIKYLITVWQPNNDVSPVSNKLGASPDILS 206
 L +IG +V+PFCRCP++ G+ ++++++V+QPNND+V+G+ G+ Q L+
 Sbjct 149 IVPFTLIGQVPIPLCKCPKSNQDREGIKYLITVWQPNNDVSPVSNKLGASPDILS 208
 Query 207 ENNYQNTAASNLVPLVPTLLDPLQIG+----SPSDGRKHRI+GLVPIIGISLQCTLLV 260
 N G N + +FV LE L O S +K R GL+ + LG C L+
 Sbjct 209 VN--GNNIQFPTD--IFVFNRLPQLSQPVVVPVTEKKERKGLITGLAVGLGCGVCL 264
 Query 261 VVSAILLVCCCKMKKSNR+AGASGATADKLIPGQVLLIPVTCGGCTKMRNSAF 303
 I++ +EAT +B T EVTK +G A+K K + BELIKQKVNHNLYK
 Sbjct 265 ----ILIGSWFREGKLNKRSSEDEDDKKRLRYKGEKGLTEMETRIADVSDCLDKYR 320
 Query 304 MYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNLYK 363
 + +EAT +B T EVTK +G A+K K + BELIKQKVNHNLYK
 Sbjct 321 VFETDELKAEATDGFENFLIGSVYKQINGQDYAIKMKKNYAEELKILQKVNHNLYK 380
 Query 364 LMGVSSDN-DNQCFFVYVYEAQNSLEELFAKSCSETSNRSTLTWCORISIAVDVSMGL 422
 L G D+ DQ+C++VEY ENGSL WL N L W R IA+DV+ GL
 Sbjct 381 LEGFCIDSDGSCYLIEYIENGSLHSLH+----NKNELNMLKRLIALDVAAGL 433
 Query 423 QYHEHAYPRIVHRTDTSNILLDSNEKAIANFSMARTFTNMM----- 467
 QYHEH +P+VH+DTSNILLDSNEKAIANFSMARTFTNMM-----
 Sbjct 434 QYHEHAYPRIVHRTDTSNILLDSNEKAIANFSMARTFTNMM----- 467
 Query 468 -----SKIDVAFAPVAILLLGLKAMMTTKEGVEVVLAKDKIWIPI--GENREKRIAK 520
 +++DVF+GVVVI+EL+G++A+ E G V LW + +D EE + +L+
 Sbjct 494 TDGVVSTRMDVFSFGVLLIELISGKEAI--DEEGRV--LMAKVSNGWDGNEKKVKRLKG 549
 Query 521 WNDPK-LDNYPIPYDIALSGLAVNCTADKLSRPTIABIVLSL 563
 +ND L ++ + + +AV C R+ +IV L
 Sbjct 550 FNDESLLRESGMSHIIHVMVAVACLHDKPAKRPMSVIVYDL 593

>ref|XP_002280070.1| G PREDICTED: hypothetical protein [Vitis vinifera]
 Length=622

GENE ID: 100264758 LOC100264758 | hypothetical protein LOC100264758 [Vitis vinifera]

Score = 348 bits (893), Expect = 1e-93, Method: Compositional matrix adjust.
 Identities = 214/590 (36%), Positives = 329/590 (55%), Gaps = 70/590 (11%)

Query 27 AQSQ-QTNGTNFSCPSN-SPPSCETVYVYISQSPNLSLTSGVNIPTDPSLIARASNLQ 84
 +G+Q + N T + C + N S C T + Y + SPNPL L S + ++ S L I + SN+
 SQAQPEPNATYPCSNALNSYPCHTFAFYATTSNFNLDLAIQGLFWWSKIMISEPNSIS 86

Query 85 HEEDKLIPGVLLIPVTCG-----TGNRSFANISYEINQCGSYFYVATTLYQNLTNWHA 139
 +G L + P + C G T S+AN+SY I GD+FY VIT + NLT +++
 Sbjct 87 SPNPLVACQSLFVPLVNCSCNSVNTTATSAIANLSYTIKSGDFFYLVSTFSLNITYS 146

Query 140 VMDLNPGLSQFTPIQIGQVPIPLFCCKCPKNQLDGRGKILYTHVQPNNDVSVFVSKLGA 199
 V +NP L L +G +V+ P+PCKCP+ QL G+ LII+V+Q+DN++ V+ LG+
 Sbjct 147 VEIVNPTLVPTLDVGKVIFFPFCCKCPNETQLANGVNFLISYVQPSNDLTVGAASLGS 206

Query 200 SPQDILSENNYGNQFPAASNLPLVPLVPTLLPOLIQ-----SPDGRKHRIQLPVIIIGI 252
 I+ N G N + +PV+ LP+ + Q + S + R G VIIG+
 Sbjct 207 DTASIIDVN--GDNITQFQT--IFVPSRLNLSQPNVTSASVTSVRKVERG--VIIGL 260

Query 253 SLG--GTLVWV--VSAILLVCCCLMKMSI-----NRASASAEATADKLISGVSGV 298
 ++C C L+V L+ + K + V L+ VS +
 Sbjct 261 AIGLGVGGLIQLVGVVYRHMVYKIEGDKERPLVGRGTGLKAEVNLIMADVSD 320

Query 299 VSKPTMYEGAILAETMNLSEQCKIGESVYKANIEGKVLAVKFKEDVTEELKILQKVNH 358
 + K + Y + +AT SE+ I SVYK +I+G+ A+K+ K + EEKILQKVNH
 Sbjct 321 LDYKVVYIEELRDATGGSFERSILQSGVYKSGIDELYAIKRMKNAYEELKILQKVNH 380

Query 359 GNLVKLMGVSBD-NDGNCFFVYVYEAENGSEELWFAKSCSETNSRSTLTWCQRISIAVD 417
 GNLV+L G D D C+VYE+ ENSL+ WL + + L W R+ IAD+
 Sbjct 381 GNLVSGECIPPDATCYLYVYFVWNSGLQWLHG-----DRDELNMKNRLRIAD 433

Query 418 VSMGLQYMHAYPAIVRIIDTSSNILLDSNFKAKIANFMSARTTTPMM----- 467
 V+ G+Y+HEH PR+V+DI SNVILL N +AKIANF +A+ N +
 Sbjct 434 VANGLYIHEHTRPVRIIDKSSNILLDSNFKAKIANFGLKSGCAITMHIIVGTQGY 493

Query 468 -----SKIDVFAFGVLIIELTGRKAMTTKNGEVNMLKDIWKIFD--QENNR 514
 +++DVF+PGVVL+EL++G+A+ E G V LW I+ + E+ +
 Sbjct 494 APEYLDGVVSTRMVDVFSFGVLIIELSGKEAV--DEEGRV--LWMSARGILEGDKDKV 549

Query 515 EERLAKKMDPK-LDNYPIDYALISLASIAVNCATDKSLSRPTIARIVLSI 563
 A+R+ WBD I+ +A+ C+D +++ +A+ C+ R++ +IV +L
 Sbjct 550 AKRWKMDMDEGLRESCEMDSVINMVAVATACHTDRPSKRFMSMDIVIAL 599

>emb|CB125950.3| unnamed protein product [Vitis vinifera]

Length=595

Score = 343 bits (881), Expect = 3e-92, Method: Compositional matrix adjust.
 Identities = 212/576 (36%), Positives = 324/576 (56%), Gaps = 69/576 (11%)

Query 27 AQSQ-QTNGTNFSCPSN-SPPSCETVYVYISQSPNLSLTSGVNIPTDPSLIARASNLQ 84
 +G+Q + N T + C + N S C T + Y + SPNPL L S + ++ S L I + SN+
 SQAQPEPNATYPCSNALNSYPCHTFAFYATTSNFNLDLAIQGLFWWSKIMISEPNSIS 86

Query 85 HEEDKLIPGVLLIPVTCG-----TGNRSFANISYEINQCGSYFYVATTLYQNLTNWHA 139
 +G L + P + C G T S+AN+SY I GD+FY VIT + NLT +++
 Sbjct 87 SPNPLVACQSLFVPLVNCSCNSVNTTATSAIANLSYTIKSGDFFYLVSTFSLNITYS 146

Query 140 VMDLNPGLSQFTPIQIGQVPIPLFCCKCPKNQLDGRGKILYTHVQPNNDVSVFVSKLGA 199
 V +NP L L +G +V+ P+PCKCP+ QL G+ LII+V+Q+DN++ V+ LG+
 Sbjct 147 VEIVNPTLVPTLDVGKVIFFPFCCKCPNETQLANGVNFLISYVQPSNDLTVGAASLGS 206

Query 200 SPQDILSENNYGNQFPAASNLPLVPLVPTLLPOLIQ-----SPDGRKHRIQLPVIIIGI 252
 I+ N G N + +PV+ LP+ + Q + S + R G VIIG+
 Sbjct 207 DTASIIDVN--GDNITQFQT--IFVPSRLNLSQPNVTSASVTSVRKVERG--VIIGL 260

Query 253 SLGCTLVVWVSAILLVCCCLMKMSLRSSASAEATADKLISGVSGVSKPTMYETGAILE 312
 ++G L L+ LK + +N L++ VS + K + Y + +
 Sbjct 261 AIG--LGGDKERPLVGRGTGLKAEVNV-----LMDVSDCLQYKVVYIEELRD 307

Query 313 ATMNLSEQCKIGESVYKANIEGKVLAVKFKEDVTEELKILQKVNHNLVLMGVSSD-N 371
 AT SE+ SVYK +I+G+ A+K+ K + EEKILQKVNHNLV+L G D
 Sbjct 308 ATGGSFERSILQSGVYKSGIDELYAIKRMKNAYEELKILQKVNHNLVLMGVSSD-N 367

Query 372 DQNCFFVYVYEAENGSEELWFAKSCSETNSRSTLTWCQRISIAVDVSMGLQYMHAYPA 431
 V+ G+Y+HEH PR+V+DI SNVILL N +AKIANF +A+ N +
 Sbjct 368 DATCYLYVYFVNGSLQWLHG-----DRDELNMKNRLRIADVANGLYIHEHTRP 420

Query 432 RIHVRDITSSNILLDSNFKAKIANFMSARTTTPMM-----SKI 470
 R+VH+DI SNVILL N +AKIANF +A+ N + + +
 Sbjct 421 RVHVRDITSSNILLDSNFKAKIANFGLKSGCAITMHIIVGTQGYIAPEYLDGVVSTRM 487

Query 471 DVFAFGVLIIELTGRKAMTTKNGEVNMLKDIWKIFD--QENNRERLAKKMDPK-LD 520
 DVF+PGVVL+EL++G+A+ E G V LW I+ + E+ +
 Sbjct 481 DVFSFGVLIIELSGKEAV--DEEGRV--LWMSARGILEGDKKAKRWKMDMDEGLRL 536

Query 528 NYYPIDYALISLASIAVNCATDKSLSRPTIARIVLSI 563
 +D +++ +A+ C+T R++ +IV +L
 Sbjct 537 ESCMDSVINMVAVATACHTDRPSKRFMSMDIVIAL 572

>gb|AA07091.1| SYM10-like protein [Galega orientalis]

Length=244

Score = 336 bits (862), Expect = 4e-90, Method: Compositional matrix adjust.
 Identities = 174/244 (71%), Positives = 207/244 (85%), Gaps = 3/244 (1%)

Query 222 VLIVPTLLPOLIQSPSDGRKHRIQ-LDVITIGISLGLTLVVVSAILLVCCCLMKMSLR 280
 +I+D I+ L I+ E G L+ +V+ +LV V CLMK IMF
 Sbjct 1 ILIPVNLKFDKLDSSSGSSSSSKLPLVIGISLGSFAFFIVLTLISLVYCYLKRMLKR 60

Query 281 SASSAEATADKLISGVSGVSKPTMYEGAILAETMNLSEQCKIGESVYKANIEGKVLAVK 340
 S S AEATADKLISGVSGVSKPTMYE +EAT +S+OCKIGESVYKANI+ +LAVK
 Sbjct 61 STSLAEATADKLISGVSGVSKPTMYEIDVIMEATNDLSQCKIGESVYKANISDRDLAVK 120



Query 341 RPKEDVTEELKILQKVNHNLVLMGVSSDNDGNCFFVYVYEAENGSEELWFAKSCSETNS 400
 +R+ AER+LII+ANGVNLVLMGVSSDNDGNCFFVYVYEAENGSEELWFAKSCSETNS
 Sbjct 121 KIKRDAEERLII+ANGVNLVLMGVSSDNDGNCFFVYVYEAENGSEELWFAKSCSETNS 179

Query 401 NS-RSTLTWCQRISIAVDVSMGLQYMHAYPAIVRIIDTSSNILLDSNFKAKIANFMSMA 459
 NS +SLTW QRI IA+DV+GLQYMHAY YPRI+HR IT+SNIL+DSNFKAKIANF

Sbjct 180 NSIVSSLTWSQRIAGMDVAVGLQVMEHTYPRIRHYITTSNIIIDGNFKAKIANFLDQ 239
 Query 460 RTFT 463
 +? ?
 Sbjct 240 KTST 243

>gb|ABR17803.1| unknown [Picea sitchensis]
 Length=536
 Score = 333 bits (855), Expect = 3e-89, Method: Compositional matrix adjust.
 Identities = 201/519 (38%), Positives = 282/519 (54%), Gaps = 65/519 (12%)
 Query 107 NAFSANTSYENQDSDYFVATILYONLTWNHAWMDINGLSQTLPICIGVPIPLCKC 166
 N S AN+Y T CD+PY +? ? +NLT + AV NP L L IG L I?+ CKC
 Sbjct 3 NYSQANVYTYTIGDFTYLLSTRKEMLETPYAVEVNTPLVNTNLIGSLATPIRCRC 62
 Query 167 PSKNGLDGRIKYLITHVQNDNVSIVSKNLGASPDILSENNGQNTFAASNLFVLIVP 226
 PS Q+ G K LIT+V PD + +S K GA Q++ S N S L L+EV
 Sbjct 63 PSNAQVNTGTRMLITYVVRHGDITLNLISQKFGADLQNLKISGINTSTLIPYSTL+LVFV 120
 Query 227 TLLEDLIQ-----SFSQGRKRRHGLFVIGISLQCTILVVSALL 267
 E L Q + +S G H +IG S+G+ VV A+L+
 Sbjct 121 SQKGVLAQPPSPSPPPPPPLVAVNNAATGSGGRLH---GAVIGASVGSSAAVCCIALLI 177
 Query 268 VCCVCLMKSNRSGSS-----AETADKLISGVSYKSTPMYGTGAILEATMN 316
 +VVEY EM SL ML E + -S+U M R+ A+DV+ GLQV+HEE P
 Sbjct 178 FCWVIRKRISYKQTSISEQRPFSDDGVGKTKSLMTGISDVCENPFMYSIDLDKATQN 237
 Query 317 LSEQCKIGESVYKANTGKVLAVKRFKEDVTEELKTLQKVNHGNLVKMGSSNDGNCFP 376
 S C I SVYK ++G+ A+K K D++ELKILQKRVN NLVKL GV ++G+
 Sbjct 238 FSPCLNTEGSIYKGTLDGRDYAIKMGKQISQELKTLQKVNHTNLVKLGWCISSEGGY 297
 Query 377 VVEYAEAGSIEELFKACSKSETSM-----SRTSLQORISIAVDVSMGLQVHEHAYFR 432
 +VVEY AE S L E L F A C S K S E T S M -----S R T S L Q O R I S I A V D V S M G L Q V H E H A Y F R
 Sbjct 298 LVVEYENSSINTWLHDEPSEVENMSPTGSSSSLSFWKTRQLVALDVANGILQVIREHTFSS 357
 Query 433 IVERDITSSNILLDSNFKAKIANFMAETTNPMMS-----KID 471
 +VRH+I SNNILL NF+AKIANF MA++ N + K+D
 Sbjct 358 VVHKDIKSSNILLDSNFKAKIANFMAKSGINALTKHIMTQCYMAPEYLADGVPKSLD 417
 Query 472 VFAGGVVLEILLTGKAKMTTKEN-----GEVVMWKDKIKFDQENREERLRKMDPKDF 527
 VEAGGVVLE++G++A++ + G+ +LW L + + E+ E+LRK+D L
 Sbjct 418 VFAGGVVLEIMSGKEATVRERQVPLAGKAGLLTQIRPLEGED-IEGKLAKWVDNRNLQ 476
 Query 528 NYVVDVLSIASLAVNCTADKSLRPTIAEIVLSLSL 566
 N Y +D + +A+H A C + +RFP+ EIV L S L
 Sbjct 477 NAYTMDSLVATIRACVEDPVARPTLPEIVYKLSNL 515

>emb|CAN66762.1| hypothetical protein [Vitis vinifera]
 Length=91
 Score = 328 bits (841), Expect = 1e-87, Method: Compositional matrix adjust.
 Identities = 203/569 (35%), Positives = 312/569 (54%), Gaps = 59/569 (10%)
 Query 27 AAGQ-QTNQNTSPSPCN-SFSCSEYVYTYISQSNFISLTVSVNIPDPSPLIARAAGNLQ 84
 Q+G N M T + C +N S C C T+ + SENEL L S+ ++P S L I+ SM
 Sbjct 27 SQAQPEANATGYPCSNALSYPCHTFATYATTSFNEGLASIGLFWFSRIMJSEPSNIS 162
 Query 85 HEEDKLIPQVLLIPVTCOC-----TGNRSFANISYENQDSDYFVATILYONLTWNHIA 139
 + L+ QO L+ P+ C C ? S+AN++Y I GD+PY V+T+ NLT ++
 Sbjct 87 SPBNPLVAGQSLFVPLNCSGNSVNATTAISYANLYTIKSGDTFLVSTFSLNLTYYTS 146
 Query 140 VMDLNPGLSQFTLPICIGVPIPLCKCPSKQLDRIKYLITHVQPNNDNVSEFVSNKLGA 199
 V +NP L L +G +V+ P+FCCKCP++ QL G+ +LI+V+Q+D++ V+ LG+
 Sbjct 147 VEIVNPTLVPTDLDDGVKRPVIFPCKCPNETQLANGVNFLSYVFPQSDMLTGVAAASLG 206
 Query 200 SPQDILSENNGQNTFAASNLFVLPVILVLPDILQIQ-----SFSQD--RKHRLGLFVITGI 252
 + + V + +AT SE+ + +PV+ L+ + G SP+ R R G IIG+
 Sbjct 207 DTASIIDVN--GDNIFQFQT--IFPVSRLENISQNPVATSFATSVRRVERKG--AIIGL 260
 Query 253 SLG-----CTLLWV--VSAILLVCCCLMKMSL-----NRSSASAEATADKLISGVSGY 298
 S+G C +L+V + + V K+K + R + L+ +VS
 Sbjct 261 SIGLVCGGILLVLLIGVWYRHYVMVERIKIEGDKERPIVGRSGSLKAEVNLMDVADSC 350
 Query 299 VSKPTMYGTGAILEATMNLSQCKIGESVYKANTGKVLAVKRFKEDVTEELKILQKRVN 358
 + + V + +AT SE+ + +PV+ L+ + G SP+ R R G IIG+
 Sbjct 321 LDKYKVGIEELRLADGSPFSRLSQSVYKSGISGLVAFDMKNAYEELMLQKRVN 380
 Query 359 NKNWLKSVSSD--NDGNCFPVYVYAEAGSIEELFKACSKSETSM-----SRTSLQORISIAVD 417
 GNIV+L G D D C +VVE+ ENOSL+ W? + L W R I+D+
 Sbjct 381 GNVLRLGFCIDPEDCATCYLYEFVENGLSQMLHG-----DRDEKLMKNRLRIAD 433
 Query 418 VSMGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFMAETTNPMMSKIDVFAFGV 477
 V+ GLQV+HEE PR+VH+DI SNNILL N +AKIANF A++ N L+ +VS
 Sbjct 434 VANGLYTHIEATRFVVRHDKISSNILLDSNFKAKIANFMAKSGINALTKHIMTQCYMAPEYLADGVPKSLD 481
 Query 478 VLLEILLGKAMTKENGVEMWMDIKMFI-----QENREERLRKMDPKF-LDNYTPIDY 534
 + + + + + G V L W L + + E+ + R+ + +ND L G +D
 Sbjct 482 ITNHIIVGTQKAEVDEEGRV--LWMSARGILEGDKVAKRVKMDMDEGLRESCSMDS 539
 Query 535 ALSIASLAVNCTADKSLRPTIAEIVLSL 563
 +++ ++A CT RP++ +IV +L
 Sbjct 540 VINWMAVATCTHROPKRRPSMVDIVVAL 568

>ref|XP_001767824.1|  predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ67338.1|  predicted protein [Physcomitrella patens subsp. patens]
 Length=688

GENE ID: 5931014 PHYPADRAFT_132645 | hypothetical protein
 [Physcomitrella patens subsp. patens] (10 or fewer PubMed links)
 Score = 309 bits (791), Expect = 8e-82, Method: Compositional matrix adjust.
 Identities = 218/631 (34%), Positives = 328/631 (51%), Gaps = 98/631 (15%)

[illegible]

>ref|XP_002311653.1| predicted protein [Populus trichocarpa]

gb|EEE89020.1| predicted protein [Populus trichocarpa]
length=524

GENE ID: 7473444 POPTRDRAFT_564909 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 308 bits (788), Expect = 2e-81, Method: Compositional matrix adjust.
Identities = 180/500 (36%), Positives = 278/500 (55%), Gaps = 56/500 (11%)

Query 109 SFANISYEINQGDSPFYVATTLYQNLTNWHAVMDINPGLSQFTLPIGIQVVIPLFCKCPS 168
S ANI+Y I G++FY V+T +QNLT + +V NP L L IG++V+ P+FCCKCP
Subject 13 SSANITYTIEAGNTFYIVSTKYFONLTTYSVELFNPTLPIELLDIGVEVIFPIFCCKCPH 72

Query 169 KNQLDRGIKYLITHVWQPNDSVFSNKLGLASPDILSEN-----YGNFTAAANLPVL 223
+ QL + YL+++V+QP+DN+S V++ G Q I+ N Y F + LP L

Query 224 I-PVTLPLDIIOSPSDGRKHRIGLPVITIGISLGCTLLVVVSAIILLVCVCCLMK----- 276

Subject 133 AQTPTVVVPSGAPPPEKTERKGVIIIGLAVLGLGIAGLLLVLVSGVWFYREGVLKKRDVEKV 192

Query	277	-----LNKSSASSAETAL-RLSSGVSVISAPFIMETGAILREITMNSLQCAIGSVIA	329
		LN + + + L++ VS + K +++ + EAT SE C I SV+K	
Subject	193	EEKRRMQLNCGSGKGLKDIEVSLMADVSDCLDKYRVFKIDELKEATNGFSNCLIEGVSFK	252

Query 330 ANIEGKVLAVKRFKEDVTEELKILQKVNHGHLVVKLMGVSSD-NDGNCVFVYYIAENGSL 386
+I G+ A+K+ K+ EELKILQKVNHGHLVVKL G D D NC++VYE+ ++GSL

Subject	233	GSINGEATIRAKAKWNAACEEDRIDYAVNHNUNVRKEGFCIDFEDANCILVETVFVDSGSH	312
Query	389	EWLFAKSCSETSNSRSTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSN	446

Sbjct 313 SWLH-----RNEKEKLSWKTRLRVAIDVANGLOQYIHEHTRPRVHVHKDIKSSNILLDSS 365

Query	449	RAAKIANSMARTINFE	SKIDVRAZGVVLELISGRA	408
		++AKIANF +A+T N++	+++DVF+FGVVLE+EL++GR+	
Sbjct	366	MRAKIANFGLAKTGCNATIMHIVGTQGYIAPEYLDAGVVSTRMDVFSFGVVLELISGRE		425

Query 488 AMTTKENGVEVVMWKDIWKIFD---QEENREERLRKWMDFK-LDNYYPIDYALSLASLAV 543
A+ E G+V LW + + + +E + +RL WMD L+ ++ ++ ++A+

Query 544 NCTADKSLSRPTIAEIVLSL 563

Subjct 482 ACLHRDPSKRPSMVDIVYAL 501

>gb|EAY87082.1| hypothetical protein OsI_08480 [Oryza sativa Indica Group]
Length=651

Score = 299 bits (765), Expect = 8e-79, Method: Compositional matrix adjust.
Identities = 196/601 (32%), Positives = 307/601 (51%), Gaps = 85/601 (14%)

Query 36 NFSCPSNSPPSCETYVTVYISQSPNF-LSLTSVSNIFDTSPLSIARASNLQHREDKLIPGQ 94
F+C +N+ C Y Y + L ++ ++F S +A A+NL L Q

subject	59	GFNFIAITTFPCPAALIRASFGGVFLFPAATGDSFPAASRFVAVHANNLSTSA-VIARRQ	97
Query	95	VLLIPVTCGCTGN--RSFANISYBINQGSFYFVATTLYQNLTNWHAVMDLNPGLSQFTL	152

Sbjct 98 PLLVLPLQCGCPSRSPNAYAPMQYQINAGDITYWIVSTTKLQNLTYQAVERVNPTLVPTNL 157

```

Sbjct 158  IG V P4FCACP+ + L+T+V QP D + ++ Q +S N Q 214
DIQIVTFFPICQCPA---EDNATALVTVMQPGDTYASITAFADVAGSLVSNLQREQ

Query 213  NFTAASNLPLVLPVT-----LLPDLIQ-----SPSDGRKRRI GLPVII 250
S+ +L+P+ LP +++ +P+ +R G+ +

Sbjct 215  GTANLSSPELPLPRKQVEMLPPIVVRNNISTTPASPPPTNPAPTVMSSNRDGVVTGL 274

Query 251  GILGCTLLVVSAILLVGCCVCKMKSLNRSASSAETADK----- 290
+ IS LAQ+ +LEA + +K+ R A C + D

Sbjct 275  AIGGVGGGLLQMLQLLGLLCKRRLAKARGARAAVASGDGCGRFTKAASGGGGGGG 348

Query 291  ---LSSGVGVSKPTMYETGAILEATMNLISGCKIKGESVYKAMIEGKVLAKRFKEQVTE 348
L+S +S + +K +++ + 2 + + I SVYKA I+G+V AVK+ K D E

Query 335  RFLVSDISELMDKYKFKVELESOTGQFDDHLIGQSVYKAYIDGEVFAVKMKWDACE 394

Query 349  ELKIKQVKNHNLVLMQVSSDND--GNCFFVVEYAENGSLLEWLEAKSCSETSNRSRTSLT 407
ELKIKQVKNH NLVK + + + G+C+ +VVEY ENGBL+ WL + + L
Sbjct 395  ELKIKQVKNHNLVLEGTFCINSETSGCYLVVEYENGSLDLWMDR-----DRARLD 448

Query 408  WKURISIAVVSMSGLQYMEHAYPRVHRDITSNLILDSNPKAKIANFEMARTTPTNP-- 466
+ R LAQ+ +LEA + +K+ R A C + D AKIANF +A+T N

Sbjct 449  WKARIRIALDIAGRLQIHEHTVMVRVKDKIKSNVLLDDMRKAIANFLGAKTCHNAV 505

Query 466  -----NMKIDVFAFGVVLIELLTKRKAMTTKENGVEVMMLKDI+ W 505
+ +K+DVEA+GVVL+EL+GR+A+ + +GE LW D

Sbjct 509  THIVGTQGYIAPEYLDGLVLTTRMDVEAYGVVLELVSGREAV--SDSGSE---PLMADAE 565

Query 506  KIFDQENR--DELRKMDPKL--KNYPIYALSLASLVNCTADKLSRPTAIEVLSL + 563
E R E R + +MDP L A E + NP LS A C + + + + + +RP+ + + +L
Sbjct 566  RLFRGKEELKARVAAMDPALAEQCTCPPSVASVAVKAKLHRDPKAKRFRKVVAYTL 625

Query 564  S 564
Sbjct 626  S 626

```

>emb|CAO02950.1| LyeM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=249

Score = 298 bits (762), Expect = 2e-78, Method: Compositional matrix adjust.
Identities = 150/245 (61%), Positives = 189/245 (77%), Gaps = 3/245 (1%)

```

Query 53  YIQSQSNPLFSLTVSNIFDPSPLSIARASNLQNEEDKLIPQVLLIPVTCOCTGNRGSFN 112
+ QSPNPLSL++S+IF+ SPL IA+ASN+ E+ KLIP Q+L+PVTCOCT N SFAN
Sbjct 1  YRAQSQSNPLFSLSNISDIFNLSPLRIKASNI EAEDKVLIPQVLLIPVTPVTCOCTGNRGSFN 60

Query 113  ISYEINQDSGYFYVATTIYQNLNWHAVMDLNPGLSOFTEPIGIGVVLPLECKCPKSNKL 172
I+V I GSD+ + + T YQNLN+ + NP LS A C + + + + + + + + + + + + + + + +
Sbjct 61  TYSYKCNLFITLSTGYQNLNWHAVMDLNPGLSOFTEPIGIGVVLPLECKCPKSNKL 120

Query 173  DAGIKYLIITHVMQPNKNSVFSVKNLIGASPDQILSENNYQNTAASNLPLVLPVTLLEPL 232
+ +GKYLIT+VMQ NDNV+ VSKK GAS + +LENN+ NFTA+M VLIPT LP L
Sbjct 121  NKGIKYLIITHVMQDNVDNLVLSGKPSGASQVEMLAENNH--NFTAASNLPLVLPVTLLEPL 178

Query 233  IQSPSDGRKRRI--GLFVITIGSLGCTLLVVSAILLVGCCVCKMKSLNRSASSAETADKL 291
Q +S+GRK L +IIGISIG + +V + IV V CLMK LNRS SS+ETADKL
Sbjct 179  DQPSNNGRSSSQNLALLIGISLGSFAFILLVTLSLVYVYCLMKRLNRDPTSSSETADKL 238

Query 292  LSGVS 296
SGVS
Sbjct 293  LSGVS 243

```

>dbj|BAI79278.1| LyeM type receptor kinase [Lotus japonicus]
Length=666

Score = 293 bits (750), Expect = 5e-77, Method: Compositional matrix adjust.
Identities = 192/636 (30%), Positives = 328/636 (51%), Gaps = 99/636 (15%)

```

Query 14  ILVYVLMFTCI-----EAQSQQTNGTNSFCSP-----NSPPSCETVYTVYSQSN 59
+L V++ + + + + +AQ + N C + NS SC+ +Y+ + S SP
Sbjct 18  LLVWLISPMISMTI--QNGEYNNKQLDCCQYNTYTGNCNVSGSYGYLTSKSSPE 77

Query 60  FLSLTSVSNIFTDPSLARASNLQNEEDKLIPQVLLIPVTCOCTGNRGSFNISYEINQ 119
+ +S+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 78  YNTPSISYLLNSTPSLVKASNNIT--DVTPIITDMVTVPTCSGGRYORHATNYLKK 136

Query 120  -GDSFYFVATLLYQNLNWHAVMDLNPGLSOFTEPIGIGVVLPLECKCPKSNKLDGRK 178
G+++ +A YQ+IT A+M NB ++ L G + +PL C CP+K Q D G KY
Sbjct 137  TGETYFIANNYYQSLITQALMAQNPDAK--NLFGADULHVLRCACPTKQSGAGFY 195

Query 179  LITHVMQPNKNSVFSVKNLIGASPDQILSENNYQNTAASNLPLVLPV--TLPDLIQ-- 234
L+H+ + + + + + Q Q +D N + + + + + + + + + + + + + + + + + + + +
Sbjct 196  LTLTVLSQSGSPDSIAEIPGVDTQSVLDANELDSKSVVYFTEFLVLPLKTEFARLQIAA 255

Query 235  -----SPSDGRKRRI GLPVIIIGISLCTLLVVSAILLVGCCV----- 273
S S + K VI+G+ +G + +V+ + LLV C
Sbjct 256  SPSPSPPPAPAGNDSSSSSKW-----VIVGVTVGVAVCLVA--LLVFLCFYNNRRRQ 308

Query 274  -----KMSLNRSASSAETADKLSGVSQVSKPTMYETGAILEATMNLIS 319
+K + + + E+ GV + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 209  PAPPPVSVKDPDSAVVMKSTPTTESWSLSGVRVYALISLKYQDGIQATKTFSE 368

Query 320  QCKIKGESVYKAMIEGKVLAKRFKEQVTEELKIKQVKNHNLVLMQVSSDNDGNCFFVY 379
+ KI SVY+A+ C NVR DV+E +L+ +NH N+ +L G + GR + +Y
Sbjct 369  ENKIKGVSRYASFGDDAAVKILNDQVSAEINLKRINHANIIRLSDGFCV--HKQNTYLY 427



Query 380  EYARNGSLKLEWLEAKSCSETSNRSRTSLTQWRISIAVDSMSGLQYMEHAYPRVHRDIT 439
I+ASN SL+WL + + S SL+M QR+ IA DV+ L YH+ + P +H++
Sbjct 428  EFAENDSLDGLWHSOKKYQNS--VLSLGMQKQIAYDADALNYLHNYTNPITHIKNLK 484

Query 440  SNNILDSNPKAKIANFEMARTTPTNP-----NMKIDVFAFGVVLIELLTKRKAMTT 471
+ R LAQ+ +LEA + +K+ R A C + D AKIANF +A+T N
Sbjct 485  SNVLLDCKFAKRYNSFLGARVMDQSGEGGFMTRHVGTQGYMPPEYISGLTIFMD 544

Query 472  VFAFGVVLIELLTKRKAMTTKEN---GEVVMWKIDWKIFDQENKPEERLRKMDPKLN 528
VFAFGVVL+EL+GR+A+ + E GE ML + + + + +N +L+R +MDP L +

```


Subject	545	VPAFGVVMLELLSGREATSSSEKNGLENGKMLSETVNHVL-EGDNVRDKLRGFMPTLRD	603
Query	529	YYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLS YP+D A S+A C A SRP I+2+++++LS	564
Subject	604	EYPLDLAYSMARIAAKRCVAHDLNLSRPTISEVIMTLIS	639

```
>ref|XP_001783589.1|  predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ51621.1|  predicted protein [Physcomitrella patens subsp. patens]
length=637
```

GENE ID: 5946784 PHYPADRAFT_152558 | hypothetical protein
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 285 bits (729), Expect = 1e-74, Method: Compositional matrix adjust.
Identities = 193/614 (31%). Positives = 310/614 (50%). Gaps = 77/614 (12%).

Query 27 AQSQQTNGTNFSCPSNSPPS---CETYVTYISQSPNFLSLTSVSNIFDTSPLSIARAS-- 81

Sbjct 2 AQQNYNDTEGYAC--NAAPSSSTSCSTFAFYRTFQAG-ESLRKVGDFYNKTA AAVANVSGM 58

Query 82 NLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSEFYFVATTLYQNLTNWHAVM 141
NL L Q L + P + C C R S + S + I + G D + F + + + T Y L T + A + M

Subject	59	NLLSTTASLRQYQALYVPLDCRLNARSQMQVSHITIVRGDTFWLLSVTEYGGTRYQAM	110
---------	----	--	-----

NP	+ L	IG	+ +P	FC	CP	+ Q	G	YL	+T	P	+ +	+S	+ G	S
----	-----	----	------	----	----	-----	---	----	----	---	-----	----	-----	---

Query 202 QDILSENNYGNFTAAASNLPLVLIPVTLLPDL-----IQSPSDG--- 239

Sbjct 179 TDLSRANNVNSSSILDVNTTLLVPLATLPPLATMDWAPVTSQPPPSPPATVASPNAAPAV 230

Query 240 -RKHRIGLPVIIGISLGCTLLVVVSAILLVVCVCLMKKSLNRSASSAETADK-----L 291
K P+ IGI++G L + + L+ + S + E + L

Sbjct 239 ITRSASQPLYTGTAVGAPGITLAADVALLLLPKASRNSTGTRPKDLTEEMKRPNMVHIEL 290
 239 ITRSASQPLYTGTAVGAPGITLAADVALLLLPKASRNSTGTRPKDLTEEMKRPNMVHIEL 290

Quely	292	13GVSG13--AFINIEIGLIEATINWSEKRIEESVIANIEGRVDAVAFREVDIEE	349
		I+G+S V KP + I AT S + I SVYK I G++A+K+ K ++T+E	
Shic*	299	IAGSDMVQSEKDWLSHEETSTACGESPEINIEGCVYKCGINGOLVAKKCMNTT	356

Query 350 LKILQKVNHGNI LVKLMGVSSDNDGNCFFVVEYAENGSL EEWLFAKSC---SETSNSRTSL 406

Sbjct 359 LKILVHNLVKLG+ N++VIEIA++GSL+L++ +SS L
LKILCQVHHSNLVKLVGLCVGGSSENLYLVYEYAKHGSLNDCLRQAAGRTTFSQSAAYL 410

Query 407 TWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTN-- 464
WC R+ IA+DV+ GL+Y+H + P VH+D+ +SNILLD NF+AK+ANF MA++ +

Subj: 419 PWCSRVRIALDVASGLEIYIHNYTNPSFVHKDVKTSNILLDENPRAKQVAFMGMAKSAASAD 478

Query 469 -----RPMSS-----RIDVFAFGVVLIELLIGRRAMIAENGVEVMD 500
 P+++ K DV+APGVV++E+L+G++A+ E E
 Blast 479 MDTLREHTCTGCVMAEYV EHCIVTUKADVAECRAHATLCKKVAUVRDEDFEEEC 520


Query 501 WKD-----TWKIFDQ--EENREERLRKWMDPKLDNYYPIDYALSLASLAVNCTADKSL 552

Sbjct 539 VKERALSDIIVDVLNAGTAE LQTEQLRKFIDPQLHSAYPIEIASIASLAMTCIDPDP 590

Query 553 RPTIAEIVLSLSLL 566
RP++ ++ +LS +

Sbjct 599 RPSMKDVTFALSKM 612

>ref|XP_002326901.1| predicted protein [Populus trichocarpa]

gb|EEE73651.1|  predicted protein [Populus trichocarpa]
length=609

0000 00

GENE ID: 7470467 POPTRDRAFT_591844 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 205.44 (220)

Score = 285 bits (728), Expect = 1e-74, Method: Compositional matrix adjust.
Identities = 185/556 (33%). Positives = 295/556 (53%). Gaps = 54/556 (9%).

Query 46 SCSTYUTYISQDNFLSLTSVNTEDSRSLIARASNLQERDEKLRGWLIRPTCCGE

Sbjct 54 SCQAFLEFKSQ-PSFNSVPSISALTSANQEELARINNVTRLSEFPTNNEVI-VFVNCFCF 111

Query 106 GNRSEFANISYEINQG-DSFYFVATTLYQNLTNWHAVMDLNPLGLSQFTLPIGIQVVIPLFC 164

Sbjct 112 GQYYQANTTIQVTTTRGTYYVIANETYEGLSTCAALKHINIH-GEYDLLPGEELQVPLRC 170

Query 165 KCPSPKQDDRGIKYLITHVWQPDNDNVSFVSNKLGASQDILSENNYGGQNFETAASNLPVLI 224
CP+ NQ+ RG KYL+T+ +DN+ ++++ S +DIL N +N T + +LI

Subjet 171 ACPLINQVIRGINILVITPESSDDNIPDIADRFVSTIRDIIDANGMEENFDIFDITILI 230

P+ P Q+ PS R + G++ C+LLV+ +V +
 Sbict 231 PLPTQPTSSOTIIHSNPNISPPSALSFRNRGSKKKHHYESAGLAAACSLLVISIITAVVFL 290

Query 271 CCLMK-----SLNRSASSAETADKLLSGVSGYVSKPTMYETGAILLEATMNLSEQCKIGES 326

Sbjct 291 SCCKTREKVSGRGRERKQAVPED-IRVELASYEQVLKVFKFEFVRKATENLSSESIRNGS 349

Query 327 VYKANIIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENG 386
 VY+ G++LAVK+ DVT+E+ IL+++NH NL+KL GV +N G ++V EY ENGS

Subjet 350 VINGEFGREILAVKMSRDVIREVNLKRNHFNLRKLGVC-ENRGCFILVLEIYMENG 400

Sbjct 409 L EWL K ET N W QRI IA+DV+ GL Y+H P VH+DI SSN+LL+
LREWLSCKKFFETGN-----WAORIQLADVANGLYYLHSFTEPAYVHKDKTSSNVLLN 462

Query 447 SNFKAKIANFSMARTFTNPMMS-----KIDVFAFGVVLIELLT 484

Sbjct 463 GNLRKIANFSLARAATSAAMTKHVVGSGIGYMAPEYVREGQVTPKIDVYAFGVILLELIT 522

Query 485 GRKAMTTRENGEVVMLWKDIWKIFDQEENREERLRKWMDPKLDNYYPIDYALSLASLAVN 544

Sbjct 523 G+ A+ T+ +G +L +I+ I+ +N+ E L +DP L ++Al LA ++V 580
GKDAVFT-QDGRALLSTETPSIMEN-KNPEVELDPFVDPAIKSGCGTNFALCLAKVSA
Query 545 CTADKSLSRPTARTV 560
C+K + R+ +E+V
Sbjct 581 CLMKCFARRPMEZVV 596

>ref|XP_002510756.1| [E] kinase, putative [Ricinus communis]

gb|EEF57943.1| [E] kinase, putative [Ricinus communis]
Length=634

GENE ID: 8269969 RCOM_1602540 | kinase, putative [Ricinus communis]

Score = 284 bits (727), Expect = 2e-74, Method: Compositional matrix adjust.
Identities = 188/575 (32%), Positives = 291/575 (50%), Gaps = 80/575 (13%)

Query 46 SCTVTVYVTSQSPNPLSLTSVSNIT--DTSPLSTARASNIQHEEDKLIPQGLIIPVTC 102
SC+Y+T+ S P + + +S+ P D+ L I A +N+ + P L IPV C
Sbjct 56 SCQSLLTFKSAAPPYTTTPTVTSYLSLQDSASLI-IASLNNISDDVSSSTFPQSQFIFVNC 114
Query 103 CGTGNRSFA-NISYEINGQDSFYF-VATTLLQNLTNHWAVMDNPGLSQFTLPIQIVVI 160
G + + N SY + E VF VA YG L+ A+M NP + L +G+ + +
Sbjct 115 SCPCQYFQGNASVTLKFSSETSYFVANDYTCGLSTCQALMSQNP-YGDRNLNLSVGRILGV 173
Query 161 PLFCRCPKSNQLDRGKLYLTHWQPNOWSYFVANKLQASPDILSENNNYQNFTAASNL 220
PL C CP NQ G +YL+T+ D S+ + G PQ IL N
Sbjct 174 PLRCACPTSNQALGFRYLLTYMTVMDTISIAELFVGRQILDANLQSTSTSIIFPT 233
Query 221 FVLIVPTLLPDLIQS-----SSDGRKHRIQLGVIGISLQCTLLVW- 262
P+L+P+T P I++ PS G + +G+ LG LL+ V
Sbjct 234 PVLPLTTPPTIKASPPPPVSPPLTLPVLSGSGSRKW---TYVGVGLAALLIFAV 290
Query 263 SAIL-----VCVCLMKSL--NRSASSAETADKLSGCVSYKSPMYETGAIL 311
S + + K+L + SA + + G + T+Y+ +
Sbjct 291 SGFLFWYPKSRKRLLTVPISKALQDSSAVPDSSTPWSRSAGVIESLITLYKFDHLQ 350
Query 312 EATMNLSECKQKISGVYKANIEGKVLAVKRFKEDVTEELIKQVNHGNIKLVKMGVSSDN 371
AT SE+ +I SVYK +G AVK K DV+ E IL+NH N++L GV
Sbjct 351 LATDYFSEKNIKSGSVYKSGFKGDAAVKVMKGDVSSSEISILKINHNIIRLSGVCV- 409
Query 372 DQNCFFVVEYAEANGSLLEWLFKSCSETSNRSRTILTWQCRISIAVDVSMGLQYMBEHAY 431
D N++VIE+AEANGSL E + N +T LFW QR+ IA DV+ L Y+H + P
Sbjct 410 DANYLVVYFAUNGSLAE-----VYGT-LFMGRVQLADVDADANLYLNHTNP 457
Query 432 RIVRDTITNSAILLDANFKAKIANFSMARTTNP-----NMGKIDVFAFG 465
+H++ +SNILLD+N +AKIANF +ART N
Sbjct 458 PYIRKLNKTSNILLDMRAKIANFLARTLQNEAEGGLLTHRVVGTQCYMAPEYMEG 517
Query 466 -NMGKIDVFAFGVILLLELTGRKAMTTKENGVEVVMKMDIKWIPQENREERLRKMWDP 524
+K+DVFAFGV++ELL+G+A T +N ML I ++ +N +L +MDP
Sbjct 518 VITPKLVFAFGVILLESKGAATYDKNAREMLASICRVL-EGDNVRHKLCEGMDP 576
Query 525 KLQNYYPDYALSLASLAWNTADKSLSRPTART 559
I YD+ A SLA LA G + +R+ + +
Sbjct 577 SLGQVPLDLAFSLAQLAQTCISHDINARPSVSGV 611

>dbj|BAI79277.1| LysM type receptor kinase [Lotus japonicus]
>dbj|BAI79287.1| LysM type receptor kinase [Lotus japonicus]
Length=667

Score = 283 bits (724), Expect = 5e-74, Method: Compositional matrix adjust.
Identities = 193/663 (29%), Positives = 327/663 (49%), Gaps = 104/663 (15%)

Query 18 VLMFTFCIIAQQG-----TNGTNFSCPSNPPSCETVTVYISQSPNPLSLTS 65
+ P R Q + + NS SC+Y+T+ S SP + +S
Sbjct 21 AMSEFMISETQAQQEVLNNQLDCCDTHNSTYGNVCSVTSQSYLTFKSSPEYTPAS 80
Query 66 VSNIFDTSPLSTARASNIQHEEDKLIPQGLIIPVTCGCTGNRSFANISYEINGQDSFY 124
+S + + +P +A++N+ + +I + + +PVT C+G R N +Y + + G++ +
Sbjct 81 ISYLLNSTPLSLVAKSNIT-DVTPIITDMTVFVTCSCSGRQHNATYLNKKTGETTP 139
Query 125 FVATVTLQNLTNHWAVMDNPGLSQFTLPIQIVVIPLFCRCPKSNQLDRGKLYLTHW 184
+A +FQ+L G +M NP + + L G + +PL C CP+Q Q D G KYL+T+
Sbjct 140 STANNYTPSTLCQALMAQNPYDAK-NLEAGDHLVPLRCACPTKRSQDAGFRYLLTYLV 198
Query 185 QPNDSNVFVSNKLGASPDQLSENNNYQNFTAASNLVPLIV-PLVTPDLIQQ----- 234
++ ++ G Q +L N P+L+P+ T P +Q
Sbjct 199 SQGESPDSTABIPGVDTSQVLDANELDSKSVYFYFTPLVLKTEPEPARIQIASPESP 258
Query 235 -----SPSDGRKHRIQLGVIGISLQCTLLVWVAILVCCVCL----- 273
S S +K + +V+ +L L V C
Sbjct 259 PPARAGNDSSSSSKK-----TVGVTVGVAVCLVW-LVWFLCFYNRRRQAPPPV 311
Query 274 -----RMSLNRSASSAETADKLSGCVSYKSPMYETGAILEATMNLSECKQKIE 371
+K + + +G + +Y+ G T +T SE+ KI
Sbjct 312 SVKDFPDSAVMSETTPTTESWLSSEGVYAEISLTAYKFIQIQATKFFSEENKIKG 325
Query 326 SVYKANIEGKVLAVKRFKEDVTEELIKQVNHGNIKLVKMGVSSDNCNCFVVEYAEANG 385
SVY+A+ +G AVK DV+ E+ +L++NH N++L G + GN +VVE+AEAN
Sbjct 372 SVYKASFQGDAAVKILNGDVSAEINLLKRNHANIIRLSGFCV-HKGWNTLYVFEAND 430
Query 386 SLEWLFKSCSETSNRSRTILTWQCRISIAVDVSMGLQYMBEHAYPVRHVRTGTSNILL 445
S++H+M QR+ IA DV+ L Y+H + P +H++ + S WLL
Sbjct 431 SLEDDHSEKKYQNS--VSLSMWQVQIAYDADANLYLNHTNPVLIHMKLQSNVLL 487
Query 446 DNEFKAKIANFSMARTTNP-----NMGKIDVFAFG 546
+ P+AK++NF +AR + +K+DV+AFG
Sbjct 488 NGKFRKAVSNFLARAMEQDGGGGQXMTIRHVVTQGYMPKYTENGLITRMDVYAFG 577
Query 477 VVILELTGRKAMTTKEN--GEVVMKMDIKWIPQENREERLRKMWDPKLQNYIPI 532
VV++ELL+G+A + GE +L + + + +N +L R +MD L + YP+
Sbjct 548 VVMLELLSGKATGNGKNGLGKRVLTSEVNVHVLGDNVDVKLRGFMQTLRDELYPL 607
Query 533 DYALSLASLAWNTADKSLSRPTARTVLSLITLQSPATLRSILTSGLDVEATQVTL 592
D A S+A +A C A SRP I+Y+ +L+S + +L+L +S +V+ ++ V+

Sbjct 608 DLAYSMETAKRCVAHDLNSRPNI SEVFWTLB---KVGSTLDMWDPSS---EVERSESVS 661
 Query 593 SIS 595
 IS
 Sbjct 662 QIS 664

>emb|CB117583.3| unnamed protein product [Vitis vinifera]
 Length=1305

Sort alignments for this subject sequence by:
 E value Score Percent identity Query start position Subject start position
 Score = 277 bits (70%), Expect = 3e-72, Method: Compositional matrix adjust.
 Identities = 382/594 (30%), Positives = 305/594 (51%), Gaps = 70/594 (11%)

Query 16	YVVMFFECIEAQSQNGTNTVSCPSNPPSCETVTVYISQSPVPLALTSVSNIFDTPFI	75
	Y ++ +TC NG N C+TY+ + +SP + ++S+ + + P	
Sbjct 705	YTVVLGYTC-----NGVN-----TTCQTYLIFRSESP-YNNVSNISDLASDP	147
Query 76	SIARASNLQHEEDKLIPOGVLLIPVTCOCTGNRFSANISYELNQGDSPFYVATTLYQNLT	135
	+A+ + + E + + +PV C C+GN S N SY + GD + +A C Q L+	
Sbjct 748	QIAQINAVT-ETATFDNKEVIVPNCNSYSGTNTSVYKNGDYPLIANNFTQGLS	806
Query 136	NHIAWMDLNPLGSQFTLPIGIVVPLFCPSKSNGLDRGIRKYLITHVQWQNDNVISFVN	195
	+A+ + NP +S L G + +D C CPAK Q D K +YL+ + + D VS +S	
Sbjct 807	TQALLNGPNSVATNLNPGTSTIVELRCACPTAKSQDAGVYLMYSYLVAYGDTVAIS	866
Query 196	KIGASPDQIISNNYQGNFTAAKNLPLVLPVTLFDLQSPDRGRKRIGLPVIIIGISLG	255
	+G + L N + T +LIP L PS + + +VI+G+ +	
Sbjct 867	ARGVDTERTEANELSEQDTINPFTLLIP-----LQNPFSBSQTIRKVVYIVGVAAQ	320
Query 256	CTLIVVVSAILLVCCOLMKSLNRSASSAET-----ADKLLSGVSGVSKPFM	904
	+S + + V K K N + +S+ + +S	
Sbjct 921	VULLFFGYVPIPKF-FRKTKKNDQIAVSESFKLEKPKVKEHEFFESISMAQSQV	979
Query 305	YETGAILEATVNSQCKIGESVYKANIEGKVLAKRKFEDVTEELIKQVNHGNVLKI	364
	Y+ + AT N S C I SVY+ I+G + A+K+ +V+ E+ +L K+NH N++L	
Sbjct 980	YKFEELQSATDNFSPCLIGSVYRGITKGLAAIKMMDGNSEIALISKINHFNIRL	1039
Query 365	MGVSSDNDGNCVVYIEYAENGSLLEWLFKASCSSETSNTSRTSITWCQRISIAVDVSMGLQ	424
	G+ NDG+ +V+EYA NGSL +W+ +N R L W QRI I+ADV+ GL Y	
Sbjct 1040	SGICF-NDGHWLVHEYAVNGSLDWTIYN-----NDRPFLVTRQIALDVAATGLN	1093
Query 425	MHEHAYPAIVQRIIDTSNLLDSNFKAKIANFSMART	461
	+H R P + +H+ +L D + +P+AKIANF AR+	
Sbjct 1094	LHIHVSFSPYIHKDKMSNVLLDGFRAKIANFDQKASAEQGGQFALTRHIVTGKGYMAP	1153
Query 462	--FTNPMS-KIDVAFGVVLELITGRKAMTTKENGVEVLMKDIWKIPQDENREERL	518
	N ++S K+DV+AFGV++E+ TG K + GE + L + + + E++ +E+L	
Sbjct 1154	EYLENGLISTKLDVYAFGVIMLEIPTG-KEVAALYGSEIHLSEVLAVAL-HEDDGKEKL	1211
Query 519	RKWMDPKLNYPIDYALISLAVNCTADKLSRPTIAEIVLSISLLTPQSPA	572
	+ +DP +E+L W QRI I+ADV+ GL YH + P VHDIT S NLLDS+FAKRI	
Sbjct 1212	GDFTDPSIDVNPYELALMIRLIDSCITKAPAGFMDIEVQSLRIIASQSA	1265

Score = 265 bits (67%), Expect = 2e-68, Method: Compositional matrix adjust.
 Identities = 173/557 (31%), Positives = 293/557 (52%), Gaps = 56/557 (10%)

Query 46	SCETVTVYISQSPNPLSITSVSNIFDTPSLIARASNLQHEEDKLIPOGVLLIPVTCGT	105
	SC+ + + +S+ P + ++S+ + + P +A+ + + E + + +PV C C+	
Sbjct 74	SCQAFILFRSEPP-YNVVSNISDLSDPSQIAQINSVD-ETATFETKEVIVPNCNSC	131
Query 106	GNRSFANI:SYELNQGDSPFYVATTLYQNLTNHIAWMDLNPLGSQFTLPIGIVVPLFC	165
	G S AN SY P G+ + +L L+ A+ + G + + +L C	
Sbjct 132	GETSQANTSVYVQGDYTLIIANNTEFGLSTCQALRSQRTSLT-NIYTGKLTVPLRCA	190
Query 166	CPKNGQLDRGILKYLITHVQWQNDNVISFVNKLQASPDQILSNNYQ-GNFTAAKNLPLVLI	224
	CP+KNG D G+KYL+ + + D VS +S + G L N QN P +	
Sbjct 191	CPTKNGSDGVGYLMYSYLVASGDYVSSIVRFQVDTGMTLEANELEQN-----PNII	243
Query 225	P-VTLPLDLQSPDRGRKRIGLPVIIIGISGLCTLIVVVSAILLVCCOLMKSLNRSAS	283
	P-TLL PS + + + +V+ + G L+ + + + + R + A +	
Sbjct 244	PTTLLIPQNLPSBSQTIRKVVYIVGVAAQSLVLLSGSVIFFKFRKTRKEDJAI	303
Query 284	S-----AETAKLLSGVSGVSKPFMTYETGAILEATVNSQCKIGESVYKANIE	333
	S + L + S + + + + AT N S C+I SVY+ +	
Sbjct 304	SESEFACEPKLEEHELESISIAQSLKVKFEELQATDNTPNCRIGESVYRGTIC	363
Query 334	GKVLAVKRKFEDVTEELIKQVNHGNLVKIMGVSSDNDGNCVVYIEYAENGSLLEWLF	393
	G + A+K+ +V+ E+ +L K+NH N++L G+ NDG+ +V+EYA NG L +W+	
Sbjct 364	GDIAIAKKMDGVSNEIALANKINHFNIRLSCFCF-NDGHWLVHEYAVNGPLTWTIY-	421
Query 394	KCSSETSNTSRTSITWCQRISIAVDVSMGLQYMHAYPAIVRHDTSSNLLDSNFKAKI	453
	+ + +E+L W QRI I+ADV+ GL YH + P VHDIT S NLLDS+FAKRI	
Sbjct 422	---NNNDGSE-IVMWRQIALDVAATGLNLYHSYTSPPYVHKDKSNGVLLDSDFRAKI	477
Query 454	ANFSMART-----FTNPMS-KIDVAFGVVLELITGRK	497
	ANF +AR+ N ++S K+DV+AFGV++E+ITG+ +	
Sbjct 478	ANGFLARSAEQGGQFALTRHIGTRGYMAPEYLENGVSTKLDVYAFGVIMLEMTGKE	537
Query 488	AMTTKENGVEVLMKDIWKIPQDENREERLKKWMDPKLNYPIDYALISLAVNCTA	547
	E GE L L L+ E + +E+L R + +DP L +P+ + A+ + L C	
Sbjct 538	VAALEY-GENHL-PDVLVAHLHEDGCKELNFDPSLNSNPYELAVIMRLIDSCIK	595
Query 548	DKLSRPTIAEIVLSLS	564
	SRP +EIV +LS	
Sbjct 596	KBPASRPDMVETVQALS	612

>ref|XP_002990805.1| [G] hypothetical protein SEIMDRAFT_11326 [Salaginella moellendorffii]
 gb|EFJ08078.1| [G] hypothetical protein SEIMDRAFT_11326 [Salaginella moellendorffii]
 Length=539

GENE ID: 9659107 SEIMDRAFT_11326 | hypothetical protein

[Selaginella moellendorffii]

Score = 275 bits (702), Expect = 2e-71, Method: Compositional matrix adjust.
 Identities = 187/552 (33%), Positives = 287/552 (51%), Gaps = 31/552 (5%)

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Query 37  FSCPSPPSPSCPTVYVYISQSPNLSLTVSVSNIFDTSPLSIARASNLQHEKDLIPQVWL 96
      +SC SNS SC+ Y V + + L+P SV P S +A AS + + L+P QVW
Sbjct 1  YSCVSNST-SCQAYAAIRALQGD--TLQSGVLRFRISVEQLAEASQIA-QSATVLPDQWL 56

Query 97  LIPVTCGCTGNRSFANISYEINQDGSFYFVATTLYQNLNWHAVMDLNPGLSQTPLPIC 156
      LIP+ C C RS N +Y I GD+ Y V+ +Q LR+ AV NP L G
Sbjct 57  LIPLNCSCASGSRQFNATYIIQSGDTLILVNSGNTFQGLTTYQVERANPLAVETNLQPGD 116

Query 157  QVVIPLFCCKPSKQLDGRKIKYLITHWQPNQDNVSVFVSNKLGASPDILLSENNYGNQFPA 216
      V + + +A+K E + + ELKIL KV+H NVKLH+G S +D P+VEYA+NGS
Sbjct 117  SIVFPIRCACPSAQAAGVTSILVYISYIWPGLDILGDIARANNVSRTRIASDNTVSGSATFL 176

Query 217  ASNLPLVILPVTLLPDLIQSPSDGRKRRILGLFVIIGISLQCTLLVVSAILVVCVCLLKK 276
      + P + +A+K E + + ELKIL KV+H NVKLH+G S +D P+VEYA+NGS
Sbjct 177  SPAAPPANPPNPNNSPSPDSSSSSGNTGM--YVGIACVAAVLLVVAALVIFYRRRRR 234

Query 277  SLNRASASAEADK-----LLSGVSGYVS--KPMYETGAILLEATHNLSQCKIGESV 327
      + ++S AE + + LL+G+ G V +P + + +AT N S I SV
Sbjct 235  KVTKASSYAEPSKIQSPHAPLACMGHGLVDSERFVPSYEELCDATNFSASHLIQSV 294

Query 328  YKANIEKVLAVKRFKEDVT--EELKILQKVNHGVLKMGVSSDNDGNCFFVVEYAEANGS 386
      Y+ + ++A+K E + + ELKIL KV+H NVKLH+G S +D P+VEYA+NGS
Sbjct 295  YAGLRKQLVAIKEMKGGTTSQELKILCKVHNSNLVKGIGISGDD-KLFLVVEYADNGS 353

Query 387  LEEWLFKAKSCETSNSRTSLTWQRIISIAVDVSMGLQYMHAYPRIVRHDTSSNILLD 446
      L SC + W R+ +A+DV+ GL+Y+H++ P VH+D+ SSNILLD
Sbjct 354  LS-----SCHNRTPAATAIWNTRLQVAMQVATGLYIHDTYKPSFVHADVSSNILLD 407

Query 447  SNFKARTANSMARTFNP--MMSKIDVFAFGVLLLELTGRKAMTTKENGVEVWLAKDI 504
      +N +AR+ANF MAR + + +X+DVAFGVLLLELTGR+H+ + G D
Sbjct 408  ANLRKAVANFQMARLYLTHGFVTFKVDVYAFGVLLLELTGREALISTGTGSEKQYIADA 467

Query 505  W-----KIFDQENRE--ELRKNMMDPKLQNYPIYDVALSIASLAVNCADKSLSPRTIAE 558
      + P + ++N E E+L W DP LDN P D AL+ +A C +RP + +
Sbjct 468  FVKLTDFGAGDNDKEIKLKHWDPILONAVMDIALNFVEVARSCVDADFDARPNMKD 527

Query 559  IVLSLSLLTQPS 570
      + LS L + S
Sbjct 528  VTFKLSKLLSS 539
  
```

>ref|XP_002974494.1| [C] hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]

gb|EFZ24716.1| [C] hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
 Length=539

GENE ID: 9657733 SELMODRAFT_11327 | hypothetical protein
 [Selaginella moellendorffii]

Score = 273 bits (699), Expect = 4e-71, Method: Compositional matrix adjust.
 Identities = 187/552 (33%), Positives = 286/552 (51%), Gaps = 31/552 (5%)

```

Query 37  FSCPSPPSPSCPTVYVYISQSPNLSLTVSVSNIFDTSPLSIARASNLQHEKDLIPQVWL 96
      +SC SNS SC+ Y V + + L+P SV P S +A AS + + L+P QVW
Sbjct 1  YSCVSNST-SCQAYAAIRALQGD--TLQSGVLRFRISVEQLAEASQIA-QSATVLPDQWL 56

Query 97  LIPVTCGCTGNRSFANISYEINQDGSFYFVATTLYQNLNWHAVMDLNPGLSQTPLPIC 156
      LIP+ C C RS N +Y I GD+ Y V+ +Q LR+ AV NP L G
Sbjct 57  LIPLNCSCASGSRQFNATYIIQSGDTLILVNSGNTFQGLTTYQVERANPLAVETNLQPGD 116

Query 157  QVVIPLFCCKPSKQLDGRKIKYLITHWQPNQDNVSVFVSNKLGASPDILLSENNYGNQFPA 216
      V + + +A+K E + + ELKIL KV+H NVKLH+G S +D P+VEYA+NGS
Sbjct 117  SIVFPIRCACPSAQAAGVTSILVYISYIWPGLDILGDIARANNVSRTRIASDNTVSGSATFL 176

Query 217  ASNLPLVILPVTLLPDLIQSPSDGRKRRILGLFVIIGISLQCTLLVVSAILVVCVCLLKK 276
      + P + +A+K E + + ELKIL KV+H NVKLH+G S +D P+VEYA+NGS
Sbjct 177  SPAAPPANPPNPNNSPSPDSSSSSGNTGM--YVGIACVAAVLLVVAALVIFYRRRRR 234

Query 277  SLNRASASAEADK-----LLSGVSGYVS--KPMYETGAILLEATHNLSQCKIGESV 327
      + ++S AE + + LL+G+ G V +P + + +AT N S I SV
Sbjct 235  KVTKASSYAEPSKIQSPHAPLACMGHGLVDSERFVPSYEELCDATNFSASHLIQSV 294

Query 328  YKANIEKVLAVKRFKEDVT--EELKILQKVNHGVLKMGVSSDNDGNCFFVVEYAEANGS 386
      Y+ + ++A+K E + + ELKIL KV+H NVKLH+G S +D P+VEYA+NGS
Sbjct 295  YAGLRKQLVAIKEMKGGTTSQELKILCKVHNSNLVKGIGISGDD-KLFLVVEYADNGS 353

Query 387  LEEWLFKAKSCETSNSRTSLTWQRIISIAVDVSMGLQYMHAYPRIVRHDTSSNILLD 446
      L SC + W R+ +A+DV+ GL+Y+H++ P VH+D+ SSNILLD
Sbjct 354  LS-----SCHNRTPAATAIWNTRLQVAMQVATGLYIHDTYKPSFVHADVSSNILLD 407

Query 447  SNFKARTANSMARTFNP--MMSKIDVFAFGVLLLELTGRKAMTTKENGVEVWLAKDI 504
      +N +AR+ANF MAR + + +X+DVAFGVLLLELTGR+H+ + G D
Sbjct 408  ANLRKAVANFQMARLYLTHGFVTFKVDVYAFGVLLLELTGREALISTGTGSEKQYIADA 467

Query 505  W-----KIFDQENRE--ELRKNMMDPKLQNYPIYDVALSIASLAVNCADKSLSPRTIAE 558
      + P + ++N E E+L W DP LDN P D AL+ +A C +RP + +
Sbjct 468  FVKLTDFGAGDNDKEIKLKHWDPILONAVMDIALNFVEVARSCVDADFDARPNMKD 527

Query 559  IVLSLSLLTQPS 570
      + LS L + S
Sbjct 528  VTFKLSKLLSS 539
  
```

>ref|XP_002977331.1| [C] PREDICTED: hypothetical protein [Vitis vinifera]
 Length=638

GENE ID: 100258108 LOC100258108 | hypothetical protein LOC100258108
 [Vitis vinifera]

Score = 272 bits (696), Expect = 8e-71, Method: Compositional matrix adjust.
 Identities = 183/599 (30%), Positives = 298/599 (49%), Gaps = 82/599 (13%)

[illegible]

>ref|XP_002269442.1| PREDICTED: hypothetical protein [Vitis vinifera]
length=632

GENE ID: 100264999 LOC100264999 | hypothetical protein LOC100264999
(Vitis vinifera)

Score = 268 bits (685), Expect = 2e-69, Method: Compositional matrix adjust.
Identities = 182/611 (29%), Positives = 306/611 (50%), Gaps = 81/611 (13%)

[illegible]

>dbj|BAI79276.1| lysM type receptor kinase [Lotus japonicus]
length=633

Score = 268 bits (684), Expect = 2e-69, Method: Compositional matrix adjust.
Identities = 204/659 (30%), Positives = 327/659 (49%), Gaps = 116/659 (17%)

Query	1	MAVEPVSDELGAQILVVLVFFTC-LEAQSQQTNGTNSFCSPNSP-PSCETVYTVIISQSP	58
		+PP AQ Y+L C S G C S +C Y+Y Q Q P	
Sbjct	14	LFIFFFFPITLGAQPTIGLTNACPRRGNSNSIRG---YTCGGSSANHCTQAYLITRTQ-Q	70
Query	59	NFSLSTNSIFPTDPSLIRG---ASNLGHEEDKLPGQVLLIPVCGCTGGRSFANIS	114
		+S+S+S+T+ A+ A N E K L + +PV C C G G A N S	

Subj	71	YNSVYSSVTLISBDAIRHLEMTSSVITFTFNKVL	-----IVPVCQSGAGCYQYNTS	125
Query	115	YEINGDSYFVATYLLITNMHVAH-DLNPGLSQFTPLGICVQPLPCKKQSNGL	V + D+ + A + + LT + A + M + NPG + I + G + + + EL + C + P + KNG +	172
Subj	126	YAFQSDTTPSIANITFEGTLTQALMHHNNIG	-----HYLHGLRGLTFCRCP+RNQ	181
Query	173	DGKLYLTHVWQDQNVSVFNKSLGSPQDISENTPAASNLVPLVLPVLLPL	-----	203
Subj	182	GRIGLYLTHVWQDQNVSVFNKSLGSPQDISENTPAASNLVPLVLPVLLPL	D + S + + X + G + S + I + N + + T + A + P + K + L + L +	236
Query	233	IQSPSDGR	-----KRLHGLVLTISGCTLLVSVYSAALLVC	269
Subj	237	NDKPSNQSTLIQSPBSSTSSPSPBSSTSSGNKNTLVVVVG	-----GVFALLVTAIVF + C	292
Query	270	VCCLMKSLNASSASATSE	-----KILGSGVSCPRPMYMETGAILLA	313
Subj	293	YTHYKXKXSSQLSVTFSEFNQIQKMGKSGDKGLSFIHQIAGSKFYVSFEELQA	K + K + S + S + + + K + + G + + + Y + I + A +	352
Query	314	TMLNSSLGSGSYKANIKGLVLAIRKFDVDEELKIQVGNHNLVNLGVSGVDF	-----	373
Subj	333	TMLNSSLGSGSYKANIKGLVLAIRKFDVDEELKIQVGNHNLVNLGVSGVDF	-----	411
Query	374	NCVFFVYEAAGSLSEWLEFKASCSSETBNSRTSLWQCRISIAVDVSMGI	Y + V + Y + N + L + D + F +	432
Subj	412	WHLTVYTAAGSLSEWLEFKASCSSETBNSRTSLWQCRISIAVDVSMGI	L + W + QRI + QAL + VAI + GIL + YLS + FSPH +	463
Query	434	VRDITLNSNTLLGDSKFIANFSMART	-----FTNFM	466
Subj	463	TRDKLSDSGVLLSIVLILKATLSIAIRSLAGVQVDEEDVPLQNTQYMAPEYEL	-----	522
Query	467	MS-KIDVTFAPGVLLSIVLILKATLSIAIRSLAGVQVDEEDVPLQNTQYMAPEYEL	K + D + V + A + P + G + V + L + L + T + G + + + A + N + K + + + ERII + + + MD	523
Subj	523	VSTKLDVYARGVLLSIVLILKATLSIAIRSLAGVQVDEEDVPLQNTQYMAPEYEL	-----KMLSGVLSAVIG + ERIKLEFMD	575
Query	524	PKLQNYVPTDIALSLASNTADKLSIRPTETLVLISLILQLQSPATILRSITSG	-----	582
Subj	576	PKLQNYVPTDIALSLASNTADKLSIRPTETLVLISLILQLQSPATILRSITSG	-----	623

[illegible]

```

>ref|XP_002532379.1| serine-threonine protein kinase, plant-type, putative [Ricinusa
Community]
>gb|EF29111.1| serine-threonine protein kinase, plant-type, putative [Ricinusa
Community]
Length=617

GENE ID: 8272991 RCOM_0411670 | serine-threonine protein kinase, plant-type,
putative [RicinusaCommunity]

Score = 264 bits (674), Expect = 3e-68, Method: Compositional matrix adjust.
Identities = 179/580 (30%), Positives = 309/580 (53%), Gaps = 74/580 (12%)

Query 37 FSCPSNPSPCCATVYVTSISQSPVSLTSGVNI FDTSPSLATARSNIQHEEDKILP-QQV 95
+ + + + + Y + C + H + C + T + G + S + + + + + + + + + + + + + + + + + + + + + +
Sbjct 47 YTC--NGKESKATLYKSGPP+VYVTSISKLTSDPLEALININSP--TVLTNKE 101

Query 96 LLDPVTCGCGNNSPANSVSYT-NGDSVSPVATYTLQINLNGWAMIDNNGSGLPTPLI 154

```

Sbjct	102	++++C+G+ AN SY I + D+++A+Y+L+ +H+M N SHFL+ VIVPILCSSSQYQYVSTIPISTYDFTAFSTAFSTLSCNMQN-RNYSFSLD	160
Query	155	GIOVVLPCSSKQKSNQIORDGIKYLITHWQNDPNMSVFNKSLGASDITLSENNYQNF	214
Sbjct	161	G++ +BL+C CP+ N+ G KYL+T+ D V+V + AS + NY F GMLSLVPLRACAPTSKSSANGKYLITLTVSVMGDKVRAVEKFNASIDV+ -NYANGF	214
Query	215	TASN--LP--VLIVSLVETLQTS-- -- -- -- --PDRCKRHGLWFL	249
Sbjct	217	TQDITLTFVPLTLPVLSTPSTKSTVIVYPPPPYFPI PVPPIRARGKILHVMV I	249
Query	250	IGISGCTILVVVSLATLVCVCLKSKSISASASRAZKATLGVSGVYSKVTPTGCA	309
Sbjct	277	IVSA+PVLVILV--LLNKSKSHSLVQREKKGKNEKLPDFDLVAVMDLAKITFFEE	334
Query	310	LEATMNSKSSQSGSYDHANKEGVLAVERKEDVTEELKILQVKNHGLMIVGMS	369
Sbjct	339	LKVAETDSSNGLDSVGVSGVIGSQVGLKSGKMSVNSVETLKHMFHLSLH+CA	393
Query	370	DNGCNFVYYEAYNSLFLFKASCKSTSNRSTSTWQRISIAIVMSGMYHERA	429
Sbjct	394	G+G +H+Y+ +NGSL+LFL++C+E +W IR IA+DV+GL Y+H ERHGVFVITLTFEYMNLSRLVLYRNKCLEA-- --SWNRKIQALDVAHGLYLHNT	429
Query	430	YPAIVRHDTSSNLTLSNFKANLHART	465
Sbjct	448	DPYYKIDSSNVLVLTAKKSTLSSASLAKSAEHWNSRLALSGKLYAPEFID	465
Query	466	--SKGIVDAFVQVILLTKRANTKMGVGLKMDIKVFLQDNEERLRKMD	523
Sbjct	508	GLTF+ID+AFGVV+EL+G+H+A+ +Z +V I+ +E N ER L+D +P+D+YAGVGLVLLTGLVEKAVMYQKRV+QLSETIISIMEE+NAEARGLQV	565
Query	524	PKDNYNIPDYDALSSIALVNCVTAQKLSRSLTAFVILSL	563
Sbjct	566	ISQIASHSEVIRVWKLISLAL+CA SRP+ALVIL ISQIASHSEVIRVWKLISLAL+CA PERSRSLAL	605

```
>ref|XP_002533278.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
gb|EF29110.1| BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
length=647
```

GENE ID: 8272990 RCOM 0411660 | BRASSINOSTEROID INSENSITIVE 1-associated
receptor kinase 1 precursor, putative [Ricinus communis]

Score = 263 bits (673), Expect = 4e-68, Method: Compositional matrix adjust.
Identities = 187/626 (29%), Positives = 314/626 (50%), Gaps = 95/626 (15%)

Query 18 VLMFFTCIEAQSQQ-----TNGTN-----FSCPSNSPPSCETYVITYISQSPNFLSL 63
+ + F C + + QQ TN TN + SC + SC+TY+T+ SQ P + ++

Query 64 TSVSNIFDTSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSEF 123

Subject	72	TSISTLLNSDPSQLS-AINSVSETATFTDNKLIVVPVNCSCSGDYQANTSYVVQAKDAP	130
Query	124	YFVATLLYQNLTNHAWMDLNPGLSOFTLPIGQIOWVPLFCKCPSKNQDRGIKYLITHV	183

Sbjct 131 FFIANNFTFQGLSTCQAINDDQNRRTVDIFPNEI-LHIPLRCACPTKNTDAGIKYLLSYL 189

Sbjct 190 VTWGDVTSAVSVKFGGNTGRSL EANGLS EQTPTIYPFTTLLIPLNPPTS NQTISP P P P P P 249

Query	236	-----PSDGRKHKRIGLPVIIIGISLGCTLLVVVSAILLVVCVC-----	272
		P++G + + V+G+ G + + I+ +	
Shot	250	ASDDDDDDDTDTDNNGSSSKKKYVVLGVGLAGIVETLGIPTLEVALFDRSRKRDEITV	308

Query 273 -----LKMKSINRSASSAETAADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESV 327
+ KSN+ E + L +S +Y+ + ATNSCI SV

Subject	310	SESFLAQSLINAKKLD--EESQDFLDVSISSIAQSIRVIRFRELEAATDNFSPSCWIRGSV	367
Query	328	YKANIEGKVLAVKRFKEDVTEELKILQKVNHGSLVKLMGVSSDNDGNCVFVVEYAENGSL	387

Subjet	368	YRGYISGDYAAIKKVNQDVSKETLLNKNVHFNLRISLQGVCSFG-GHWLYVLEYEAANGAL	426
--------	-----	---	-----



Sbjct 427 +W++ ++N L+W QR+ IA+DV+ GL Y+H P +H+DI SSN+L+DS
SDWIYY-----SNNEGFLSWTQRVQLALDVATGLNYLHSFTSPPHIHDKIKSSNVLIDS 481

```
Query 448 NPKAKIAISMART-----FTNPMS-KIDVFAPGVVIE 481
          *F*AKIAN+MAR+ N++S K+DV+AFG++++E
Sbjct 482 DPAKIANLAMARSTGGDGEFALTRHIVGTKGYMAPEYLENGLVSTKLDVYAFGIMLE 541
```

Query 482 LLTGRK--AMTTKENGVEVVLWKDIWKIFDQEEENREERLRKWMDPKLONYYPIDYALSLSA 539
 + +TG++ A+ T+EN + + D+ + + + + L++++DP ++ +P ++ +L+
 Subject 540 MVTGGRK--AMTTKENGVEVVLWKDIWKIFDQEEENREERLRKWMDPKLONYYPIDYALSLSA 539
 + +TG++ A+ T+EN + + D+ + + + + L++++DP ++ +P ++ +L+ 539

Query 540 SLAVN-CTADKLSRPTIAEIVLSLS 564
 ++ C ++ E T S I S

Subject 598 VRMIDSCLNKNPADRPAMDEISQSL8 623

ref|XP_002522569.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor,
putative [Ricinus communis]
gb|EF39869.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor,
putative [Ricinus communis]
length=624

GENE ID: 8259229 RCOM 1014860 | BRASSINOSTEROID INSENSITIVE 1-associated
receptor kinase 1 precursor, putative [Ricinus communis]

Score = 262 bits (669), Expect = 1e-67, Method: Compositional matrix adjust.
Identities = 180/601 (29%), Positives = 304/601 (50%), Gaps = 69/601 (11%)

Query 25 IEAQSQQTNGTNTFSCPSNSPP-----SCETYVTYISOSPNFLSLTSVSNIFDTS 73

[illegible]

```
>emb|CBI40796.3| unnamed protein product [Vitis vinifera]
length=680
```

[illegible]

Score = 77.4 bits (89), Expect = 5e-12, Method: Compositional matrix adjust.
Identities = 43/98 (43%), Positives = 66/98 (67%), Gaps = 5/98 (5%)

Query	469	KIDVFAGVGVLEILLGRKAMTT--KENGEVVMWMDIKFIQDQENREERLRKMMDPKL	526
Sbjct	31	KLIDFAGVGVIILELLGKAAPGQRKEGG--LLSVSTNEVL-QCDNVRRKLRGIDPDL	87
Query	527	DNYDIYDALSLASLANCTADKLSRPTIAIVLISLS	564
Sbjct	88	VYD A SVA IA C A RFT RFT LLS AHVDTYSALSLASLANCTADKLSRPTIAIVLISLS	125

```
>ref|XP_002510333.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
gb|EFP52520.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
```


Length=637

GENE ID: 8260932 RCOM_1593420 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 258 bits (658), Expect = 2e-66, Method: Compositional matrix adjust.
Identities = 164/557 (29%), Positives = 294/557 (52%), Gaps = 53/557 (9%)

Query 46 SCETYVTVYISQSPNPLSLTVSNIFDTSPLSIARASNQLQHEEDKLIPIGOVLLIPVTCGCT 105
+C+ ++ + S+ P+ S ++S + S +AR +N+ + + +V+ +PV+C C

Subject	54	TCQAFLIISRPP-YDSAPTISALTSASQEELARFNVTGLSEFPLNKEVI-VFVSCSCL	111
Query	106	GNRSPANISYEINQGSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCK	165

Sbjct 112 G ANS+++ S++A+ Y+L+ ++ N +F L +G ++ +PL C 170
GQYYQANTSQVASDHSYFTIASQTYEGLSTCASLKKANI-YGEFDLALGAELQVPLRCA

Query 166 CPSKNQILDRGIKYLITHVWQPNNDNVSVFVSNKLGASPODILSENNYGQNF⁺TAASNL⁺LPVLIP 225
CP+ +Q+ KYL+T +D++ ++ + S + I+ N ++ T + +LIP
Sh16+ 171 CPMASQVWNEFKYLITPDTSESDTAATAPENMVEKSTINDAGICDPTDPTDIT 230

Query 226 VTLLPDLIQ-----SPSDGRKRNRIGLPVIIGISLGCTLLVVVSAILLVCV 270

Sbjct 231 +T P Q SP D R+ + L +GI+ C+LLV+ +I+V +
 LTTEPSNSQTIHENPTEVSPPLASPPDNRRSKRKLKYGITACSLVL--SIIVIL 288

Query 271 CCLMKMSLNR--SASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVY 328
 L+ ++ + + + L ++ ++ + +ATN S + I S+Y
 Subject 289 ETLVDPRKHEDPNNRPPGGLDRIATGSEGVV KVDGIPEUKKATMPSSKTKGSLV 348

Subject	289	FLLRKDRHHKFPENRRREQEDLRLEIASVQVLKVFGLEEVKKATDNFSSKHIKGSLY	348
Query	329	KANIEGKVLAVKRFKEDVTEELKILQKVNHGNIIVKLMGVSSDNDGNCFFVVEYAENGSL	388

Sbjct 349 G+LA+K+ DV++E+ IL+++NH NL+KL GV +N G ++ +EY +NGSL+
WGEFNGQILA IKMNRDVSKEVNIIKRINHFNLIK LHGVC-ENLGCFYLFFEYMKNGSLQ 407

Query 389 EWLEAKSCSETSNRSTSLTWCRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSN 448
 EWL + + + +W QRI IA+D++ GL Y+H P VR+DITS+ILLD+N
 Subject 409 EWLEKREDFEHC-----GRIQRIQAI DNGLEYPVHCEDDCAVDYDITSCILLDNN 461

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Subject 408 EWLSREREDVG-----SWNQRIQIALDIANGFLPYLHSFTEPACVHRKDITSGHILLDNN 461
Query 449 FKAKIANFSMARTFTNPMMS-----KIDVFAFGVVLIELLTGR 486

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Sbjet 462 LRAKIANFSLARAAANAVLTKHIEGTRGYMAPEYVQAGQVTPKIDVYAFGIVLLELITGK 521

Query 487 KAMTTKENGVEVMLWKDIWKIFDQENREERLRKWMMDPKLDNYPIDYALSASLAVNCT 546
A+ ++ G+ +L K I+ + ++ EN E L ++DP AL IA +++ C

Subject 522 DAVFMRD GKETLLSKAIFSVMEK-ENAEAEAFVIDPSFTGGGRQSKLALRLARVSLACL 579
Query 547 ADKSLSRPTIAEIVLSL 563

Sbjct 580 TQVPARRPSMGVEVSTL 596

>ref|XP_002269408.1|  PREDICTED: hypothetical protein [Vitis vinifera]

length=638

GENE ID: 100242712 LOC100242712 | hypothetical protein LOC100242712
[Vitis vinifera]

Score = 256 bits (653), Expect = 9e-66, Method: Compositional matrix adjust.
Identities = 171/574 (29%), Positives = 292/574 (50%), Gaps = 66/574 (11%)

Query 46 SCETYVITYISQSPNFLSLTSSVSNIFFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT 105
SC+ ++ + S+ P + ++S+S++ + P +A+ +++ E + +++PV C C+

Subject	54	SCQAFLLFRSEPP-YNDVSSISDLGSDPSQLAQINSVD-ETATFETKKEVIVPVNCSCS	111
Query	106	CNRSEANTSVRTNOCDSFEVETATLIVNTNTHAUMDINBCISQETIPICTQWUTPLECK	165

Query	106	GNSFANLAEYEINQGGDSYFFVATLLYNLNNHVAHMDLNPGLSQFTLPFGIQVVPFLPCK	165
		G S A N S Y + G D + + A + + L + A + L + + G + + P L C	
Sbjct	112	GEFSQANTSYVWQHGDTYLLIANNTFEGFLSTCQALRSQRTSLTT-NIYTGKLTVP L R C A	170

Query 166 CPSKNQLDRGIKYLITHVWQPNNDNVSVSNKLGASPDILSENYYG-QNFTAAASNLPVLI 224
CP+KNO D G+KYL++++ D VS +S + G L N ON +LI

Subject	171	CPTKNSQSDVGKYLMSYLVASGDYVSSISVRFGVDTGMTLEANLSEQNPNIYPFTTILI	230
Query	225	DAWYIYDDYEQS	265

Query	225	PVTLTPDIQS-----PSDGRKRRIGLPLVIGISLGCITLLVVVSAIL	266
		P+ LP Q+	
		+ + V+G+ G L++ ++	
Sbjct	231	PLQNLPLSSSQITVPPPPPPPPSPPPPTAVSSPSKSLKKTWVYVVVGWVAGSALVLLFGSVI	290

Query 267 LVCVCLMKMSLNRSASS-----AETADKLLSGVSGYVSKPTMYETGAILEATMN 316
K + A S E + L + S + Y + + + A T N

Subjct 291 FFKFFRKRKKTDPDIAISSEFEACEKPLKEEQHEFLISSIAQSLKVKYFEEIQLSATDN 350

Query 317 LSEQCKIIIESVYKANIEGKVLAVRFKEDVTTELKIIQKVNHGNIIVKLMGVSSDNDGNCF 376
S C+I SVY+ I+G +A+K+ +V+ E+ +L K+N+ N++L G+ NDG+ +
Sbjct 351 FSPNCRIKSGSVYRGTIKGLDLAAIKMDGVSNEIALLNNKIHNFVIRLSGICF+NDGHWY 409

Query 377 VVVEYAENGSLLEENLFAKSCSETSNRTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHR 436
+V+VYE NG I. +M++ + +SR I. MORT TA+DW+ GL Y+H + P VH+

Sbjct 410 TVTEIA NG L TATTT + TSK L W QRI LA+DV+ GL IYH + P VHT
LVHVEAVNGPLTDWIY----NNNDSDRF-LVWVQRIQIALDVATGLNLYLHSYTSPPYVHK 464

Query	437	DITSNIILDSNFKAKIANFSMART-----FTNPMMS-KI	470
		DI S N+LLDS+F+AKIANF+AR+ N++S-KI	
Subject	465	DIKSGNVLLDSDFRAKIANFGLARSAGOGQFALTRHIIGTRGYMAPEYLNGLVSKL	524

Query 471 DVAFPGVVLIELLTGRKAMTTKENGVEVVLWKDIWKIFDQEEENREERLRKWMDFKLNYY 530
DVAFPGV+++F+ITG++ E GE + I D+ E + +E+R + +D+ I Y

Sbjct 525 DV+AFGV++E+LIG++ EGE+L D+ E++E+LR++DF L Y
 582 DVYAFGVLMLEMLTGKEVAALYE-GENMHL-PDVLVAVLHEGDGKEKLRNFIDPSLSGNY

Query	531	PIDYALSASLAVNCTADKSLSRPTIAEIVLSLS	564
		P++ A+ + L +C SRP + EIV +LS	
Subject	583	PLEIAIVMIRLIDSCLKKSPASRPDMVEIVALS	616

DOI: 10.1002/anie.201100000

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>ref|XP_002281880.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=622
```

GENE ID: 100248852 LOC100248852 | hypothetical protein LOC100248852
[Vitis vinifera]

Score = 254 bits (650), Expect = 2e-65, Method: Compositional matrix adjust.
Identities = 188/608 (30%). Positives = 305/608 (50%). Gaps = 83/608 (13%)

identities = 100/000 (50%), positives = 500/000 (50%), gaps = 00/000 (1%)

<http://blast.ncbi.nlm.nih.gov/Blast.cgi>

Query 23 TCIRAQSQQTGNTGNSFCPS--NSPPS-----CETVYTYISQSNPLSLTSSVS 67
 Sbjct 16 +C AQ + +C +S PS C + + + S+ P +S+ +S
 SCINAGQGVSONVIMCNDGSSPSRFLFYCNGLYSQCAQLLPKSEKPP-VNSGVPTIS 74

Query 68 NIFDTPSLSIARASNLQHEEDKLIP-QVLLIPVTCGCTGNRSPANISYEINQDSYFY 126
 Sbjct 75 MLMSNSPGLARINSVK--TLTFVFTPKKEVIVPNCSCGLGQYQANTTFHIDNQQTYYI 132

Query 127 -ATTLYONLTNHWAMVDNLGSLQFTLPIGIQVPIPLCKCKPKNQLDRGILKYLTHWQ 185
 Sbjct 133 IGNNTYQGLSTCDLIRAN-RYSEFSLPGLELHVLRACATHEQAQENCTYLLTSSVS 191

Query 186 PNDNVSVFNKLGASPDILSENNY--QGNFTAASNLPLVILFVTLPLDILQ----- 234
 Sbjct 192 KEDNFTPTIGERISVSAKSIADANGLISENPFIPTFTTILPIKTEPLSQTTHATQPV 251

Query 235 -----PSDGRKRRIGLPWIGISLGCTLL--VVVSAILLVCCCLMKMSIRBSA 282
 S S K R I L G I G C L L V + B + L K
 Sbjct 252 LDPPPTSSSSSSSRKRIYLG--GLAAGCFLGSPVIFVFLFYKPKSKVPPVHGK 309

Query 283 SBAETADKLIGSVGSYKSPMYETGAILEATMNLSECKIGESVYKANIEQKVLAVRF 342
 Sbjct 310 TKSVLPEDLIVELASVDVPRVETKELAKATNFBKGRIRKQCVFRAELGREIVAKRM 369

Query 343 KEDVTEELKILQKVNHNGLVKLMGVSDNDGNC--VVEYAENGSLLEWLFKASCSSETSN 401
 Sbjct 370 KVDISEEVNINKNLNHLNKLIGVC--KNGSCFYLVFEYMENGLSLEWLFKES----- 421

Query 402 SRTSLTWCQRIASIVDSMGLQYHHEAPRIVHRDITSSNILLSDNFKAIANFSMART 461
 Sbjct 422 SNBSGWSBKRIQIALDVAHLHYHNTKATPVHRHKKSSNILLTNLRAKIANLSART 491

Query 462 -----FTN-----MMSKIDVFAFGVLELITGRKMTTKENG 485
 Sbjct 482 AVKGAATHNLMLVYVTRGYMAPEYIEAGSITPKVDVYAFGVMLELITGDAVII--QNE 540

Query 496 EVVWLKWDINKIFQDENREERLRKWDPKLDNYPIDYALSASLAVNCTADKLSRPT 555
 Sbjct 541 EEVLLEAMISIMER-GNAEIELGHFLDPCLLGNNGIESATRIAKLSACLTQRARRPS 599

Query 556 IAEIVLSL 563
 Sbjct 600 MGEVVSLE 607

>ref|XP_002310777.1|  predicted protein [Populus trichocarpa]

gb|EEE91227.1|  predicted protein [Populus trichocarpa]

Length=643

GENE ID: 7477999 POPTDRAFT_563086 | hypothesized protein [Populus trichocarpa]
 (10 or fewer PubMed links)

Score = 253 bits (645), Expect = 6e-65, Method: Compositional matrix adjust.
 Identities = 171/585 (30%), Positives = 280/585 (47%), Gaps = 82/585 (14%)

Query 46 SCETVYISQSNPLSLTSSVS NIFDTPSLSIARASNLQHEEDKLIPQVLLIPVTCGCT 105
 Sbjct 53 SCQALYIFRSQPP-YSTVASISTLLGSDPSQLSINSVS-ETTSPTNQLVLVFNCSGS 110

Query 106 QNRSPANISYEINQDSYFYATTLYONLTNHWAMVDNLGSLQFTLPIGIQVPIPLCK 165
 Sbjct 111 GDYFQANASYIVQSGNTFELIANNTYQGLSTQCAIRN-EKGTTRTVNIFAGETLIVPLRCA 169

Query 166 CPKKNQLDRGILKYLTHWQ PNDNVSVFNKLGASPDILSENNYQ-NFTAASNLPLVIL 224
 Sbjct 170 CPKKNQDGLKYLTHWQVLTVDVSIAGVRFQADIGRALEANSEINSENPFIPTFTLIL 229

Query 225 FVTLPLDILQ-----PSDGRKRRIGLPWIGISLGCTLLVVVSAL 265
 Sbjct 230 PLKNPPTSSQTVVPPPPSPSPSPSPSPSNDKSNKTIWYFVFGVAGGVILTLVIGTI 289

Query 266 LLVCCCLMKMS-----INRSASSATADKLLGSGVGSYKSPMYETGA 309
 Sbjct 290 IFPMLFRKSKKQPGPIVQSQFEAHEKPLNRKLD--EEPQDLLESVYSIAQSKIVNYED 347

Query 310 ILEATMNLSECKIGESVYKANIEQKVLAVRFKEDVTEELKILQKVNHNGLVKLMGVSS 369
 Sbjct 348 LXAATDNFSPFWIKSGVFRGLINGDFALIKRMNDGVSKEIDLLINKNLSIRLSGVCV 401

Query 370 DNDGNCVVEYAENGSLLEWLFKASCSSETSNRSRTSLTWCQRIASIVDSMGLQYHHEA 429
 Sbjct 408 -NDGHWLVLYEYAANGSLSDMIYV-----SSNEGKFLKWTQRIQATDVATGLNLYHSFT 461

Query 430 -YPRIVHRDITSSNILLSDNFKAIANFSMARTFTN----- 465
 Sbjct 462 YP VBIQITSSNILLSDNFKAIANFSMARTFTN----- 520

Query 466 --MMSKIDVFAFGVLELITGRK--AMTTKNGEVMLWMDINK-IFQDENREERLR 519
 Sbjct 521 NGIOTKLDVYFAGILTLEMTGKVAALYRENERL----SEVLNGLSEGGGLEESLS 576

Query 520 KWNMDPKLDNYPIDYALSASLAVNCTADKLSRPTIAEIVLSL 564
 Sbjct 577 QLIDPSMGQNYPSGLAVMLVRLDSCLNKNPAGPAMDEIVQSLS 621



gb|AB259612.1| LYK4 [Glycine max]

Length=633

Score = 253 bits (645), Expect = 8e-65, Method: Compositional matrix adjust.
 Identities = 191/629 (30%), Positives = 322/629 (51%), Gaps = 77/629 (12%)

Query 7 SLLTGAQILYVIMFTTCIEAQSQQTGNTGNSFCPSNPPSCETVYTYISQSNPLSLTSSVS 66
 Sbjct 20 SLLGQGP-VIGLGTVAC-PRGNKNSIRGYCT-NGAANSQSYLTFRSQ-PYNSWKTI 75






[illegible]

```
>ref|XP_002327712.1|  predicted protein [Populus trichocarpa]
gb|EER75190.1|  predicted protein [Populus trichocarpa]
length=630

GENE ID: 7464252 POPTRDRAFT_796841 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)
```

Score = 249 bits (635), Expect = 9e-64, Method: Compositional matrix adjust.
Identities = 178/583 (30%), Positives = 290/583 (49%), Gaps = 80/583 (13%)

[illegible]

```
>ref|NF_001058110.1|  Os06g0625200 [Oryza sativa Japonica Group]
dbj|BAD35689.1|  receptor protein kinase-like [Oryza sativa Japonica Group]
dbj|BAF37734.1|  receptor protein kinase-like [Oryza sativa Japonica Group]
dbj|BAF2024.1|  Os06g0625200 [Oryza sativa Japonica Group]
gb|EAZ37689.1|  hypothetical protein OsJ_2029 [Oryza sativa Japonica Group]
Length=630
```

GENE ID: 4341567 Os06g0625200 | Os06g0625200 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

Score = 242 bits (618). Expect = 8e-62. Method: Compositional matrix adjust.

Identities = 171/568 (30%), Positives = 291/568 (51%), Gaps = 66/568 (11%)

```

Query 46  SCTEYVYTIQSQPNFLSTSVSNIFDTSPLSIARASNLQHEEDKLPQGVLLIPVTCGCT 105
      + SV+ S P + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 56  SCTAYLTFRSDPP-----LSVAYLLNATTSAAVAANSVPLAVSPVDGTLVLPVPCSC 109

Query 106  GNRSAF-----NISYEINQDSGFYPVATTLYQNLTNHWAVMDLNPGLSOFTLPICQVWIP 161
      NR+ N +Y I + D+F+ +A Q LT + + + NP + I + + P
Sbjct 110  -NRATGYQHTTYATQELDTFLFIANNTPQGLITTYQSIANNPASEAMSVPVINGPLAV 168

Query 162  LPCKPSKNGLDRIKYLITRWQNDNVSFVSKNLGASPDILSENNGYQNTAASNLP 221
      L E CDS P + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 169  LACACPSBATTG--INNLITVYVCGEINVTSLARRNSTHGDVLAANTLLVLVHPHHR 226

Query 222  VLIPVTLLEDLQSPDRQKHRI-----GLPVIIGISLGLCT--LVVSAIILVVCVCL 273
      V+ + T + + + P + + K + GL +GI +GC + V A+ L+
Sbjct 227  VLIANTITIS--TTPESQKQFVSSPCNGLAGLIGVCGGCSAAVAFLVLRWR 284

Query 274  NKSILNRSASAEATADKLISGVSGYVSKPMYETGAILEATMNLSECKT--GESVYKAN 331
      + + + S + ET L+ + V G V Y I AT + E+ + + G SVY+ A
Sbjct 285  RAPVGDSSCAKET--PLVAAVRGAVETLAAYSDIETATAGFAEERVAAGSSVTRAV 342

Query 332  IEGKVLAVAREK--EDVTEELKILQKVNHGMLVRLMGVSDNDGNCFFVVEYAENGSL 388
      I G+ AVRK + DV E+ + VYNE LV+ I G+ + D + + V E+EN+ I L
Sbjct 343  INGEAFVARKVAAGDQVVRGEVDVLGRVNSHGLVRLRGLCAND--DTYLVLFEAENGSL 401

Query 389  EWLFAKSCSETNSRSTLTWCQRISIAVDVSMGLQYMEHAYPRIVHRDITSSNILLSDN 448
      EWL S + R L W QR+ +A+DV+ GL YH P VH++ S N+LLD+N
Sbjct 402  EWLHFGSAAALC--RRVLGQRVRLVALDVAGGLNLRHFTNFPYVHKLNLSGNLLDAN 459

Query 449  FKAKIANFMA-----RTFTNP-----MMSKIDVPAFGV 477
      + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 460  LNAKVSLLGAFARAVAVAGDSDIALMTHTVGTGILAFYELEGLISPRDLVDFSGV 519

Query 478  VLEILLTGR-KAMTTKNGEVVMLMKDIKRFQDENREERLRKMMDPKLNYYPIDAL 536
      + +LL+G+ A T + +G+ +LW+ + D + + +L+ +MD+P L +YPI A
Sbjct 520  IQLLELLSGKTAATVTDGDDGNMLLQAADGLVD--DGAFKLRAPMDPQLQGRHYPCVAS 578

Query 537  SLASLAVNCTADKLSRPTAEIVLSLS 564
      +A+LAV C A + +RP+ E + +LS
Sbjct 579  AVAALAVNCVAREPARPMEEVFTLS 606

```

>ref|XP_002307830.1|  predicted protein [Populus trichocarpa]

gb|EEE94826.1|  predicted protein [Populus trichocarpa]

Length=659

GENE ID: 7479122 POPTRDRAFT_662283 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 239 bits (611), Expect = 7e-61, Method: Compositional matrix adjust.
Identities = 170/591 (28%), Positives = 290/591 (49%), Gaps = 86/591 (14%)

```

Query 46  SCTEYVYTIQSQPNFLSTSVSNIFDTSPLSIARASNLQHEEDKLPQGVLLIPVTCGCT 104
      + SV+ S P + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 58  SCQSYLTFRSMPPNVSFVLIAYLLGVQSATRIASNNLSNDTATIPNTQVVPVNCSC 117

Query 105  TGNRSFA-NISYI--NQDSGFYPVATTLYQNLTNHWAVMDLNPGLSOFTLPICQVWIP 162
      + + N +Y+ + + + + + VA YQ LT + +M NP L +G+ + IPL
Sbjct 118  YARQQYQHNSTYQLKDKSBETYPVANNTYQGLTQOGLSNQNP-YGRNLLSLGLTLQIFL 176

Query 163  FCKCPKNGLDRIKYLITRWQNDNVSFVSKNLGASPDILSENNGYQNTAASNLP 222
      C CP+ NQ GI +L+T+ + D+H+ + + G Q +L N + + + + + B+
Sbjct 177  RCACPTNNGASGINLILPMVWQDSISIAQLFVDVMDQVLDANKLSSNNIFPTPT 236

Query 223  LIPVTLLEDL-----QSPS-----DGRKHRIGLPVIIGISLGLCTLVVSA 264
      L+P A P + + + + + + H+ + +G+ +G L+ + + A
Sbjct 237  LVPLPTEPTKIQPSAAPPAPSPQTPNVSVGGSSDHK--ALYVGVGIGAAFLILLFA 293

Query 265  ILLVVCVCLMKSLNRSASAEATADKLISGVSGYVSKP-----ALYVGVGIGAAFLILLFA 303
      K + + + S+ + + L S + + P T
Sbjct 294  AFGFLFWHRGRKQKPKVTSSE-FETLPSVSTDTVLVPSVNNKSNWLSHDARYAIESLT 352

Query 304  MYETGAILEATMNLSECKTGESVYKANIEGRVLAVKRFKEDTEELKILQKVNHGMLV 363
      +Y+ + AT + + + T SVY+ + +G AVK K DV+ E+ I+ + +H + + + +
Sbjct 353  VYKYEDLQVATGYPAQNLKQSVYRGSFGKDTAAVVKVGDVSEINILKMNHSNVR 412

Query 364  LMGVSDNDGNCFFVVEYAENGSLLEWLFAKSCSETNSRSTLTWCQRISIAVDVSMGLQ 423
      L K + +GN + +VVEYA+NGSL +WL + +N L W QR+ IA DV+ L
Sbjct 413  LSGFCL-HEGNTLYVVEYADNGSLDNL-----HNNIYRLIAWKQRVRIAYDVADAN 465

Query 424  YMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP-----ALYVGVGIGAAFLILLFA 465
      Y+H + P H+ + + +SNILLD+ +AK+ANF +ART N
Sbjct 466  ILYNNTNPSYTLKRAKVAANLILDANLEMGDGGGLQTRHVVGTQGYL 525

Query 466  -----MMSKIDVPAFGVLIBLITGRKAMT--KENGDEVVMLMKDIKRFQDEN 513
      + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 526  APEYIENGVTIPKGLDVFAGVLMLELGSKEAATAIDKIASG-DLLVMIMRVL-EGSN 583

Query 514  REERLRKMMDPKLNYYPIDALISLASLAVNCTADKLSRPTAEIVLSLS 564
      E+L + +DP L + YP+D A S+LA C +RP+ + + + LS
Sbjct 584  VREKLSAPLQCLRDQYPLDFAFSAQLAKSGVEHDLNTRSPMPQVFMML 634

```

>emb|CA002961.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=131

Score = 238 bits (606), Expect = 2e-60, Method: Composition-based stats.
Identities = 109/130 (83%), Positives = 120/130 (92%), Gaps = 0/130 (0%)

```

Query 411  RISIAVDVSMGLQYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKI 470
      RI+ A+ DV+ GLQYMEH YPR+HRDIT+SNILL SNFKAKIANF MART TN MM KI
Sbjct 1  RITAMDAVLGLQYMEHETPRIIHRDITSSNILLGSNFKAKIANFSMARTFTNSMMKI 60

Query 471  DVPAFGVLIBLITGRKAMT--KENGDEVVMLMKDIKRFQDENREERLRKMMDPKLNYY 530
      DVPAFGVLIBLITGRKAMT--KENGDEVVMLMKDIKRFQDENREERLRKMMDPKLNYY

```

Sbjct 61 DVAFPGVLLIELLTGKKAMTTKNGEVLWKKDFKIFDLEGNREERLRKMMDPKLSFY 120
 Query 531 PIDYALSLAS 540
 PID ALSIAS
 Sbjct 121 PIDNALSLAS 130

>ref|XP_00259540.1| [E] ATP binding protein, putative [Ricinus communis]
 gb|EEF50927.1| [E] ATP binding protein, putative [Ricinus communis]
 length=681

GENE ID: 8271475 RCOM_1677900 | ATP binding protein, putative [Ricinus communis]

Score = 236 bits (602), Expect = 7e-60, Method: Compositional matrix adjust.
 Identities = 192/638 (30%), Positives = 304/638 (47%), Gaps = 101/638 (15%)

Query 25 IFAQSQQTNGTNSFCPSN--SPSCCTVTVYIISQSNFLSLTSGVNIIDTSPSLIARASNL 83
 Sbjct 30 ILCSETTSPDASGYRCNINGSQDCKATFAL--LSTNYSFSSLSNLSFYLGNNFVIAEANGF 88
 Query 84 QHEEDKLIQGVLLIPVTCGCTGNRSFANISYEINQGDSEFYVATTLYQNLNHWAMD 143
 Sbjct 89 SADTEFLPKQDPLILPIDCKCNINFFRAVVKTKITKGNFYGIASRI--EOLITCKAIQEN 147
 Query 144 NDELQSETLPIGIVIPLEFCCKPSKNQLDRGKYLITLHVQPNDRNVSFVSNKLGAAPQD 203
 Sbjct 148 NLGVSPWNLADKARLLVLRKCAQPSQVTLATLAFSLSYFVSGDTIGNIAIKFNTTPEA 209
 Query 204 ILSENNYG--QNTAASNPLV---LIPVTLPLD--IQSPSDGRK--HRIGLEVI----- 247
 Sbjct 208 IISANNRSIANFKPENILVPLASLLIPNREPALGSLAKFREPSFPRESSIPVINPHKKK 267
 Query 250 -----TGISLQCTLLVV-----VSAILLVVCCVLAAMKSLNR-----SASSATAD 289
 Sbjct 268 SKMMIGVYIATGVVGGATATVAALFVLQKKKKQNLKQDGPQLQSLSVRTTSE 327
 Query 290 KLLS---GVSGVSKFTM-----YETGAILEATMNLSECKQKESVYKANIEG 334
 Sbjct 328 KKVSEFGSQDQLNDIITTPRNKRVIVENYVEELRKATDEFPSSSLIDGVSUYGRING 387
 Query 335 KVLAVRKFKEDVTEELKILQKVN---GNVLKMLGVSSDNDGNCPPVVEYAEAGSLEW 390
 Sbjct 388 KNLAKRKFKETGILIDFBSFQNAHTRHPNIRILQCTLSESGSGDPIFVEYAKNSLQW 441
 Query 391 L-----FAKSCBETSNSRSTLSQVRIASIVAVMGLQYMHIEHAYPRIVHRDITSS 447
 Sbjct 448 LHGGLAMKNQFIASC-----YCLFTWNRKILCLODAVALQYMHIMHNSVYHRVNRK 501
 Query 442 NILLDSNFKAIANFSMARTT-----TNP-----MMSKIDVF 473
 Sbjct 502 NIFLDEEFNAKGNFGMARCIIEGDTQNTIEHSTNFSWSLGLYLAPEYHQGVSPCIDIF 561
 Query 474 AFGVLLIELTGRKAMTTKNGEVLWKKDFKIFDQENREERLRKMMDPKLSFY 532
 Sbjct 562 AFGVLLIELTGRKAMTTKNGEVLWKKDFKIFDQENREERLRKMMDPKLSFY 532
 Query 533 DYALSLASLAVNCTADKSLRPTIAEIVLSILLTQPS 570
 Sbjct 621 DTAVTLANLARSCEVEEPLRPNAGELVKRLSRLVES 658

>ref|NF_566689.2| [E] CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase [Arabidopsis thaliana]
 dbj|BAF2788.1| [E] chitin elicitor receptor kinase 1 [Arabidopsis thaliana]
 length=617

GENE ID: 821717 CERK1 | CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 229 bits (583), Expect = 1e-57, Method: Compositional matrix adjust.
 Identities = 165/543 (30%), Positives = 273/543 (50%), Gaps = 77/543 (14%)

Query 81 SNLQHEEDKLIQGVLLIPVTCGCT--GNRSFANISYEINQGDSEFYVATTLYQNLNHW 139
 Sbjct 71 SNLQHEEDKLIQGVLLIPVTCGCT--GNRSFANISYEINQGDSEFYVATTLYQNLNHW 139
 Query 140 VMDNLSDELQSETLPIGIVIPLEFCCKPSKNQLDRGKYLITLHVQPNDRNVSFVSNKLGA 199
 Sbjct 130 IQRANP--FPATNIPSLATNLVNVNCSGDES--VSKDPLGLVTLPLRPEDESLSIARSSGV 196
 Query 200 SPQDILSENNYGQNTAASNPLV---LIPVTLPLD--IQSPSDGRKHRIGLFPVILGSLG 256
 Sbjct 188 S--ADILQRYNPGVNPNSNGIYVYFGRDPNGAFPPFKSSKQDQ---VGAGVIAGIVIGV 242
 Query 257 TLVNVVVALIVVCCVLAAMKSLNR-----ETADKLLSGVSG----- 297
 Sbjct 243 IVALLL--ILFVIVYAYRNNKSGDSFSSIPSLTKADHASSTSLQSGSLGAGVSPGIAA 301
 Query 298 -VYSKPTMYETGAILEATMNLSECKQKGE-----SVYKANIEGKVLAVRKFKEDVTE--- 348
 Sbjct 302 ISVDKSVSEFLEELAKATDNFSLFKIGQGGFVAVYAELEGRAKAAIKMDMEASKQFIA 361
 Query 349 ELKILQKVNKNLNVKMLGVSSDNDGNCPPVVEYAEAGSLEWLFKSCBETSNSRSTLSJTW 408
 Sbjct 362 ELKILQKVNKNLNVKMLGVSSDNDGNCPPVVEYAEAGSLEWLFKSCBETSNSRSTLSJTW 408
 Query 409 CQRIASIVAVMGLQYMHIEHAYPRIVHRDITSSNILLDSNFKAIANFSMARTT----- 460
 Sbjct 413 TRVQIALDSARGYLEIHETTPVYVHRIDKSNAILIDQKFRKAVDFGLTKLTVGGSSA 472
 Query 461 -----TTTNMMSKIDVAFPGVLLIELTGRKAMTTKNGEVLWKKDFKIFDQENREERLRKMMDPKLSFY 506
 Sbjct 461 -----TTTNMMSKIDVAFPGVLLIELTGRKAMTTKNGEVLWKKDFKIFDQENREERLRKMMDPKLSFY 506

Sbjct 473 TRGAMSTGYMAPETVYGEVSAKVDDVYAGVVLVELISAKGAVVKMT--EAWGEPRGLVG 530
 Query 507 IPDQ---EENKEERLRKNNPKLNNYIPIDYALSLASLVNCTADKSLSRPTIAEIVLSL 563
 +P+ + +EE LDK +D+L+ + YP+ + + S F SL++S +A+ + +S+ +V++L
 Sbjct 531 VFEESEKTEKDEALRKILIDPLRGDSYPPDSVYKMAELGKACTQENAGLRFPMRYIVVAL 590
 Query 564 SLL 566
 S L
 Sbjct 591 STL 593

>ref|XP_002300098.1|  predicted protein [Populus trichocarpa]
 gb|EEE84903.1|  predicted protein [Populus trichocarpa]
 Length=680
 GENE ID: 7467712 POPTDRRAFT_641782 | hypothetical protein [Populus trichocarpa]
 (10 or fewer PubMed links)
 Score = 224 bits (572), Expect = 2e-56, Method: Compositional matrix adjust.
 Identities = 192/629 (30%), Positives = 296/629 (47%), Gaps = 87/629 (13%)
 Query 25 IEAQSQQTNGTNFSCPSNS--PPSCSTYTVYISQSNFLSLTSVSNIFDTSPLSIARASNL 83
 +P+ + +EE LDK +D+L+ + YP+ + + S F SL++S +A+ + +S+ +V++L
 Sbjct 32 LSCQTPSDAGCYGHCNGLQDCKQCTVATL-LHTSYSSLSLSNLFYGLGRVIAATNGF 90
 Query 84 QHEEDKLIPOGVILFVTCGCTGNRSFANISYEINGDSFVATVILYQNLNNWAVMDL 143
 +L Q LIP+ C C G A ++ +G+BFY +L+ +L+ A+ +
 Sbjct 91 SANTFELPKDQPLILPIDCKNGGFFQALVTKTIGKESFYSIKSL-EGILTCKAIRK 149
 Query 144 NFGSLQFTLPIGIVQVLEPCCKPCNKQLDRGKILYITHVQNDNVSFVSKNLGASPD 203
 NPG+S L +Q+ +DL C CFS ++ + L+++ D +S +K +P+
 Sbjct 150 NFGISPENINGVQLQVPLRCACFBSSTEVILATRLILLSYFVSAGDTISNLAIKPTTFFA 209
 Query 204 ILSENNGY-QNPTAASNLFPV---LIPVTLLEPL--IQSPSDGRKH--RIGLPVI----- 249
 T S NN M F S +P+ LIP+ P L + P+ + E LEVI
 Sbjct 210 ITSANNRSLTTFKPTSLVPLTSLILPGLQKPTLQPLAKPNFNLIPASSLFPVPHKKR 269
 Query 250 -----IGISLQCTLLVV-----VSAILVCCVCLMKKSLNRS-----SSAETADK 290
 IG+ + T VV ++A LV K +L++ A S T+DK
 Sbjct 270 SKMKRIGVYIAVTVGAVGVSTIAAAAFVILQKKKKQVLSKAEADTELQQLISVTRTSDK 329
 Query 291 LLS-----GVSGVSKPTMYETGAILE--ATMNLSECKIGESVYKANIIEKVL 337
 +L ET +E AT + + +L SVY + GK L
 Sbjct 330 KVSFDDSQNHFDQITDTTGKVFYVYVYVEELKATEDFNSSNQIGESVYGRGLNKL 389
 Query 338 AVKRFKQWTE--ELKILQKV--NNGNLVKMLGSSSDNGCNFVYVEAENGSLSEWL-- 391
 A+K+ + + EL + Q +H N++++G + P+V+EY+NGSL+WL
 Sbjct 390 ATRKQVETISKVELGLQDATHHNPNIIRVVGCTLSEGDPSLFVEYAKNGSLKDWLIG 449
 Query 392 --FAKSCSETNSRSTSLTWQRISIAVDVSMGLQYMEHAYPIVRHIDTSSNILLDSNFK 450
 A ++ LTW QR+ I +DV+ LQYHM +P VHR+ S NI LD P
 Sbjct 450 GLAMKNQIASCYFLTNQRLKILQDVAVALQYMHIMHPSVYHRNKSNRNPILDEEFN 509
 Query 451 AKIANFMSMARFP-----TKS-----NMKSIDVAFQGVLEILL 483
 AKI +F +F +F TNP + S D+P+GCVL+E+L
 Sbjct 510 AKIGFMGACGVDDTKEPDPFNSNPFASWSGLYLAPEAQCVSSSTDFISFGVIVMEVL 569
 Query 484 TGRKAMTF-KENGK-VVMLWKDQKWFQDQENREERLRKNNPKLNNYIPIDYALSLASL 541
 +G+ +T +NGE + L K I I EN+E LR+W+D + Y D A +LA++
 Sbjct 570 SQQTPIRFNDNGGSIWLSKKIKSL-LSENADE-LREWIDSAMGENSYSTDEATLANI 627
 Query 542 AVNCTADKSLSRPTIAEIVLSLITQPS 570
 A CT + RPT EIV L L + S
 Sbjct 628 ARACTEDPSLRPTSGEIVKLLRIVES 656

>ref|XP_002263070.1|  PREDICTED: hypothetical protein [Vitis vinifera]
 Length=676
 GENE ID: 100264694 LOC100264694 | hypothetical protein LOC100264694
 (Vitis vinifera) (10 or fewer PubMed links)
 Score = 224 bits (571), Expect = 3e-56, Method: Compositional matrix adjust.
 Identities = 182/667 (27%), Positives = 303/667 (45%), Gaps = 91/667 (13%)
 Query 1 WAFVFSVLISQAQLVYVFFTC-----IEAQSQQTNGTNFSCPSNS--PPSCSTYTVYIS 55
 +A+ +L+L+L+++ + + + + C N S C T++P
 Sbjct 1 MAALINNFYLRALFLFVSTLQGLSCLSETSSRDASGYCNGSGKQCTGCTFALLAT 7
 Query 56 QSNFPLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPOGVILFVTCGCTGNRSFANIS 115
 S + SL ++S IA A+ + + L LIP+ C C A++
 Sbjct 61 NS-YYSSELENLFYLAIDRFLIAEANGFSADTELLPYNLPLIPICCKAGGFFQAEILK 119
 Query 116 EINQSDSFVATVILYQNLNNWAVMDLNNGLSQFTLPIGIVQVLEPCCKPCNKQLDRGK 175
 +G+GR+ +A+L+L+ +A+ +NF+ + +L + + + +EP+ C CFS +L+L+
 Sbjct 120 TTIEGSEFTGIAESL-EGILTCKAIRERNPFIQWGLADKVALILPLRCACTSSSELIGE 178
 Query 176 IKVILTVFVQNDNVSFVSKNLGASPDILSENNGY-QNPTAASNLFPV---LIPVTLLEPL 231
 K L+++ D V ++K + + I+S NN G S FV LIP+ P
 Sbjct 179 TKLLSYFVSAGDTVPSLAKEFTNTSAILSANNRSGATRLGSLAPVSSSLIPLRDKFT 238
 Query 232 LIQSPSDGRKHRIQLPV-----IGISLQCTLLVVSAITLL 267
 L SP+ R+ +GLD + + + + +G++G++ + + + + +
 Sbjct 239 L-GSPAKFPENLGLSATSPVFNPHKKTKMKMKIGVYIAVGVYAGVSAVAIAAVLVTH 297
 Query 268 -----VCVCLMKKSLNRSASAEADTKLLSGVSGVSKPTMYETGAILE 312
 L +++ + S E L + + + + E T +L+
 Sbjct 298 KKKKKQYAKMGSDVQLGLSLVSTSEKKVSEFGSDPIDQIDSTPHKIVVETVYTMLE 357
 Query 313 ---ATMNLSECKIGESVYKANIIEKVLAVKRFKQWTE--ELKILQKV--NNGNLVKML 365
 AT+ + I SV+ + GK LA+K + E + +H N++L+L+
 Sbjct 358 IAKATEDFNSSNLIIGSVFGRGLNKLAKHTHPEATSKIEPGLFDATHHNPIMRIL 417
 Query 366 GVSSNDNGCNFVYVEAENGSLSEWL--FAKSCSETNSRSTSLTWQRISIAVDVSMGL 422
 G C LNK + + + +EY+NGSL+WL +L TW QR+ I +DV+M L
 Sbjct 418 GTCLNKGDSYLFYKAYAKNGSLKDLGGGLAMKLSQFASCYCFLTNQRLKILQDVAVAL 477

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Query 423 QYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 465
Sbjct 478 QYMH + P VHR+I S NI LD - P AKI NF MAR F +
QYMHMHPCYVHNKSNRPIFLKSENAKIONFCMARCPCDDAEDSQPYSTASMSKGYL 537
Query 466 -----MMSKIDVFAGGVVL+ELLTGRKAMTKKEN--GEVVMWKIDIKWIFDOENR 514
Sbjct 538 APEYLHQGIIISPTLDIAYGVVLLVLEISGKTPITRADDKGGGRVWLPEKISILGSENTE 597
Query 515 REERLRKMMDPKLNYYPIIDYALSLASLAVNCTADKLSLRPTIAEIVLSLITQSPATPL 574
Sbjct 598 E LR WMD L Y D A++LA LA CT + SRP+ EIV IS L + P
E--LRWMDLSALGENYSFDAITLANLARVCTDENPCSRPAGETVEKLSRLVEQLPEGE 655
Query 575 ERSLTSS 581
Sbjct 656 QFSICES 662

```

>emb|CBI40054.3| unnamed protein product [Vitis vinifera]
Length=672

Score = 224 bits (570), Expect = 4e-56, Method: Compositional matrix adjust.
Identities = 175/644 (27%), Positives = 300/644 (46%), Gaps = 67/644 (10%)

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Query 1 MAVFVSLTLGAQLVYVLMFFTC----IEAQSQQTNGTNSFCSPN-SPPSCETVYTIYS 55
Sbjct 1 MA + L A L++++ T + + + + C N S C T + +
MAALINNFYDALPFLTIVFVTLQGLSLCSTSSRDASGYCNGSGKQCGTFAILLKT 60
Query 56 QSNFPLSLTGSNIFDTPSIIARASNLQHEEDKLI PGQVLLIPVTCOCTGNRSFANIS 115
Sbjct 61 NS--YSSLEFNLSFYLGIDRFLAEANGTSADTELLPYNLPLLIPIECKAGGFAELTK 119
Query 116 EINGGDSFYFATTLQNLTNW+HMDLNPGLSQFTLPIGIQVVLPLFCCKPSKNQLDRG 175
Sbjct 120 TTIEGSEFFGIAESL-EGLTTCARERNPISIQWGLADKVRLLIPLRCACPFSSSLIQE 178
Query 176 IKYLLTHVWQNDNVSVFNKLGASQDILSENYY-QNFTAAENLP-VLIPVTLLEPLD 232
Sbjct 179 TKLLLSYVSGDGTVPISLAFKFNNTTSAIISANNRSGATLRLGLAPENLGLPATSIPVI 238
Query 233 IQSPSDGRKHRLGVII-QISLGCTLLVVSAIL-----VCVCCLMK 275
Sbjct 239 NPHKKTKMKKIGVYIAGVGAVGASVAIAAALVIRWKRKKQAYKMGDVELQQLGLSV 298
Query 276 KSLNRSASSAETADKLLSGVSGYVSKPTMYETGAILE---ATMNLSEQCKIGESVYKANI 332
Sbjct 299 RTTSEKKVSPFESQDPIQI IDSTPHKIVVETVYTHLRLKATDENPSSNLTGSVPHRGL 358
Query 333 EGKVLAVKRFKEDVTE--ELKILQKV--NHGNILVKMGVSSDNDGNCFFVVEYAENGSL 388
Sbjct 359 NGKNLAIKRTHPEAISKTEFGLFHDATHHHPNIMRLGTCLNEGDSYLIPEYAKNSLK 418
Query 389 EWL---FAKSCSETSNRSLSLITWCQRIISIAVDVSMGLQYMHAYPRIVHRDITSSNILL 445
Sbjct 419 DWLHGGGLAMKSQPTASCYCFLTNWQRLRLICLDVAMALQYMHMHPCYVHNKSNRIFL 478
Query 446 DSNFKAKIANFSMARTFTNP-----MMSKIDVFAGGVVL 479
Sbjct 479 DERENAKIONFCMARCPCDDAEDSQPYSTASMSKGYLAPEYLHQGIIISPTLDIAYGVVL 538
Query 480 IELLTGRKAMTKKEN--GEVVMWKIDIKWIFDOENREERLRKMMDPKLNYYPIIDYALS 537
Sbjct 539 LEVLISGKTPITRADDKGGGRVWLPEKISILGSENTE--LRWMDLSALGENYSFDAIT 596
Query 538 LASLAVNCTADKLSLRPTIAEIVLSLITQSPATLERSLTSS 581
Sbjct 597 LANLARVCTDENPCSRPAGETVEKLSRLVEQLPEGEQFSICES 640

```

Select All Get selected sequences Distance tree of results Multiple alignment

APPENDIX B

BLAST

Basic Local Alignment Search Tool

[Edit](#) and [Resubmit](#) [Save Search](#) [Strategies](#) [Formatting options](#) [Explain](#)

SEQID48 (598 letters)

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

* 833458
ic|33458

Description

SEQID48

Molecule type

amino acid

Query Length

598

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.24+ Citation

References

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Reference : [compositional scoring matrix adjustment](#)

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#)

Search Parameters

Search parameter name Search parameter value

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Database

Database parameter name Database parameter value

Posted date	Sep 26, 2010 5:43 PM
Number of letters	4,071,357,309
Number of sequences	11,921,515
Entrez query	none

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.318422	0.267
K	0.132723	0.041
H	0.387286	0.14

Results Statistics

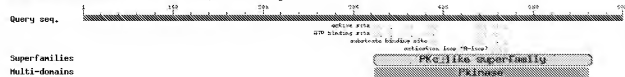
Results Statistics parameter name Results Statistics parameter value

Length adjustment	144
Effective length of query	454
Effective length of database	2354659149
Effective search space	1069015253646
Effective search space used	1069015253646

Graphic Summary

Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



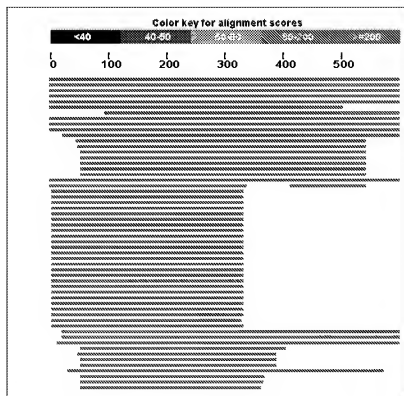
Super-families

Multi-domains

Distribution of 102 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer PubChem BioAssay

Accession	Description	Max score	Total score	Query coverage	E value	Links
ABQ08609.1	NFR5a (Glycine max) >gblADJ19105.1 Nod-factor receptor 5A [Glycine max] >gblADJ19108.1 Nod-factor receptor 5A [Glycine max]	1238	1235	100%	0.0	
AGJ18109.1	Nod-factor receptor 5A [Glycine max]	1230	1233	100%	0.0	[a]
AGJ18102.1	Nod-factor receptor 5A [Glycine max]	1233	1231	100%	0.0	[a]
AGJ18112.1	Nod-factor receptor 5B [Glycine max]	1166	1106	100%	0.0	[a]
ABJ18111.1	Nod-factor receptor 5B [Glycine max]	1193	1103	100%	0.0	[a]
AGJ17310.1	truncated Nod-factor receptor 5A [Glycine max]	1007	1037	83%	0.0	[a]
ABQ08613.1	NFR5b [Glycine max]	987	957	84%	0.0	
CAE02953.1	SYM10 protein [Pisum sativum] >emb CAE02594.1 SYM10 protein [Pisum sativum]	892	899	100%	0.0	
CAE02956.1	SYM10 protein [Pisum sativum] >emb CAE02596.1 SYM10 protein [Pisum sativum] >gblADB45277.1 Nod factor recognition protein [Pisum sativum]	899	895	100%	0.0	
CAE02995.1	Nod-factor receptor 5 [Lotus japonicus] >emb CAE02598.1 Nod-factor receptor 5 [Lotus japonicus]	876	875	100%	0.0	[a]
ABF02224.1	Nod factor perception protein [Medicago truncatula]	864	864	96%	0.0	
CAE02992.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	761	761	100%	0.0	
CAE02993.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	754	754	82%	0.0	
CAE02970.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAE02934.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAE02935.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAE02938.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAE02939.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAE02952.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. longicaulis] >emb CAE02955.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAE02957.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	747	747	81%	0.0	
	>emb CAE02956.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAE02987.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAE02971.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAE02972.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAE02973.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	745	745	81%	0.0	
	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	743	745	81%	0.0	
	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	744	744	81%	0.0	
	LysM-domain containing receptor-like kinase [Medicago truncatula]	743	741	81%	0.0	
CAE02968.1	LysM type receptor kinase [Lotus japonicus] >dbj BAI79285.1 LysM type receptor kinase [Lotus japonicus]	704	704	100%	0.0	[a]
AGJ18109.1	truncated Nod-factor receptor 5A [Glycine max]	696	695	56%	0.0	[a]
BAG08514.1	Nod factor receptor protein [Glycine soja] >dbj BAG085149.1 Nod factor receptor protein [Glycine soja] >dbj BAG085156.1 Nod factor receptor protein [Glycine soja] >dbj BAG085160.1 Nod factor receptor protein [Glycine max] >dbj BAG085161.1 Nod factor receptor protein [Glycine max] >dbj BAG085162.1 Nod factor receptor protein [Glycine max] >dbj BAG085165.1 Nod factor receptor protein [Glycine max] >dbj BAG085168.1 Nod factor receptor protein [Glycine max] >dbj BAG085171.1 Nod factor receptor protein [Glycine max] >dbj BAG085174.1 Nod factor receptor protein [Glycine max] >dbj BAG085177.1 Nod factor receptor protein [Glycine max] >dbj BAG085179.1 Nod factor receptor protein [Glycine max] >dbj BAG085180.1 Nod factor receptor protein [Glycine max]	675	675	54%	0.0	
	Nod factor receptor protein [Glycine soja]	676	674	54%	0.0	
	Nod factor receptor protein [Glycine soja]	675	673	54%	0.0	
	Nod factor receptor protein [Glycine max]	672	673	54%	0.0	[a]
	Nod factor receptor protein [Glycine max]	673	673	54%	0.0	
BAG085170.1	Nod factor receptor protein [Glycine max]	672	672	54%	0.0	
BAG085166.1	Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG085168.1	Nod factor receptor protein [Glycine max]	672	672	54%	0.0	[a]
BAG085164.1	Nod factor receptor protein [Glycine soja] >dbj BAG085145.1 Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG085147.1	Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG085152.1	Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG085175.1	Nod factor receptor protein [Glycine max]	672	672	54%	0.0	
BAG085172.1	Nod factor receptor protein [Glycine max]	671	671	54%	0.0	
BAG085157.1	Nod factor receptor protein [Glycine soja]	671	671	54%	0.0	
BAG085159.1	Nod factor receptor protein [Glycine soja]	671	671	54%	0.0	

BAG085176.1	Nod factor receptor protein [Glycine max]	670	670	54%	0.0
BA0465153.1	Nod factor receptor protein [Glycine soja]	669	669	54%	0.0
BAG08155.1	Nod factor receptor protein [Glycine soja]	669	669	54%	0.0
BA0465150.1	Nod factor receptor protein [Glycine max]	669	669	54%	0.0
BAG08173.1	Nod factor receptor protein [Glycine max]	669	669	54%	0.0
BAG08181.1	Nod factor receptor protein [Glycine soja]	667	667	54%	0.0
BA0465155.1	Nod factor receptor protein [Glycine max]	665	665	54%	0.0
BAG08166.1	Nod factor receptor protein [Glycine max]	660	660	54%	0.0
BA0465147.1	Nod factor receptor protein [Glycine soja]	659	659	54%	0.0
XP_002269472.1	PREDICTED: hypothetical protein [Vitis vinifera] >emb CB17584.3 unnamed protein product [Vitis vinifera]	654	654	96%	0.0
XP_002532280.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29112.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	638	638	96%	0.0
KF_002316178.1	predicted protein [Populus trichocarpa] >gb EEE90648.1 predicted protein [Populus trichocarpa]	614	614	97%	1e-173
CA020256.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	459	499	58%	4e-139
CA020246.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	434	454	56%	2e-134
CA020242.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	461	481	56%	1e-133
CA020236.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	477	477	55%	2e-132
XP_001468266.1	hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor] >gb EER95234.1 hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]	441	441	90%	2e-121
CA020233.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	439	436	52%	6e-120
CA020229.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	433	433	52%	4e-119
CA020224.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	427	427	51%	2e-117
AA0818120.1	Putative protein kinase [Oryza sativa Japonica Group] >gb ABF94815.1 Protein kinase domain containing protein [Oryza sativa Japonica cultivar-group] >gb EAE28175.1 hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]	426	426	93%	3e-117
EAY8155.1	hypothetical protein OsJ_10648 [Oryza sativa Japonica Group]	428	426	93%	6e-117
CA020216.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	422	422	51%	6e-116
CA020212.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	418	418	51%	9e-115
XP_002517429.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF45192.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	366	366	86%	5e-99
XP_002286079.1	PREDICTED: hypothetical protein [Vitis vinifera]	353	355	89%	8e-96
AA070791.1	SYM10-like protein [Galega orientalis]	361	351	40%	2e-94
CB026349.1	unnamed protein product [Vitis vinifera]	346	345	89%	1e-92
AB0811803.1	unknown [Picea sitchensis]	343	343	76%	3e-92
CA0849742.1	hypothetical protein [Vitis vinifera]	338	338	89%	1e-90
XP_002311503.1	predicted protein [Populus trichocarpa] >gb EEE9020.1 predicted protein [Populus trichocarpa]	324	324	76%	2e-86
CA020206.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	313	313	40%	6e-83
EAY81592.1	hypothetical protein OsJ_08480 [Oryza sativa Japonica Group]	313	313	88%	6e-83
XP_001707624.1	predicted protein [Physcomitrella patens subsp. patens] >gb EDQ67338.1 predicted protein [Physcomitrella patens subsp. patens]	302	302	91%	8e-80
BA173276.1	LysM type receptor kinase [Lotus japonicus]	297	297	92%	2e-78
XP_002326803.1	predicted protein [Populus trichocarpa] >gb EEE73651.1 predicted protein [Populus trichocarpa]	292	292	86%	8e-77
XP_001733589.1	predicted protein [Physcomitrella patens subsp. patens] >gb EDQ51621.1 predicted protein [Physcomitrella patens subsp. patens]	291	291	90%	2e-76
BA173277.1	LysM type receptor kinase [Lotus japonicus] >dbj BA179287.1 LysM type receptor kinase [Lotus japonicus]	286	286	87%	4e-75
XP_002516758.1	kinase, putative [Ricinus communis] >gb EEF52943.1 kinase, putative [Ricinus communis]	283	283	85%	5e-74
XP_002522689.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF39868.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	280	280	86%	3e-73
XP_002380609.1	hypothetical protein SELMOORRAFT_11326 [Selaginella moellendorffii] >gb EFJ08078.1 hypothetical protein SELMOORRAFT_11326 [Selaginella moellendorffii]	280	280	89%	3e-73
XP_002277301.1	PREDICTED: hypothetical protein [Vitis vinifera]	280	280	91%	4e-73
XP_002874654.1	hypothetical protein SELMOORRAFT_11327 [Selaginella moellendorffii] >gb EFJ24716.1 hypothetical protein SELMOORRAFT_11327 [Selaginella moellendorffii]	279	279	89%	7e-73
CB017583.1	unnamed protein product [Vitis vinifera]	277	277	88%	3e-72
XP_002519283.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF52520.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	276	276	86%	5e-72
BA173275.1	LysM type receptor kinase [Lotus japonicus]	276	276	91%	7e-72
BA173284.1	LysM type receptor kinase [Lotus japonicus]	276	276	91%	8e-72
AB039612.1	LYK4 [Glycine max]	270	270	96%	5e-70
CB06786.1	unnamed protein product [Vitis vinifera]	269	269	82%	1e-69
XP_002269442.1	PREDICTED: hypothetical protein [Vitis vinifera]	268	268	88%	1e-69
XP_002532279.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29111.1	265	265	90%	2e-68

serine-threonine protein kinase, plant-type, putative [Ricinus communis]									
XP_002372788.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EF29110.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	265	265	89%	2e-68	G			
XP_002372788.1	PREDICTED: hypothetical protein [Vitis vinifera]	263	263	86%	4e-68	UG			
XP_002372788.1	predicted protein [Populus trichocarpa] >gb EEE75190.1 predicted protein [Populus trichocarpa]	258	258	86%	2e-66	UG			
XP_002372788.1	predicted protein [Populus trichocarpa] >gb EEE91227.1 predicted protein [Populus trichocarpa]	254	254	86%	2e-65	UG			
XP_002372788.1	PREDICTED: hypothetical protein [Vitis vinifera]	253	253	86%	4e-65	UG			
XP_002372788.1	ATP binding protein, putative [Ricinus communis] >gb EEF50927.1 ATP binding protein, putative [Ricinus communis]	253	253	88%	4e-65	G			
XP_002372788.1	Osl6g0825200 [Oryza sativa Japonica Group] >dbj BAD35889.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAD37734.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAF20204.1 Osl6g0825200 [Oryza sativa Japonica Group] >gb EA237689.1 hypothetical protein Osl_22029 [Oryza sativa Japonica Group]	251	251	86%	3e-64	UG			
XP_002372788.1	predicted protein [Populus trichocarpa] >gb EEE94826.1 predicted protein [Populus trichocarpa]	248	248	86%	2e-63	UG			
XP_002372788.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	240	240	21%	4e-61				
XP_002372788.1	predicted protein [Populus trichocarpa] >gb EEE84903.1 predicted protein [Populus trichocarpa]	238	238	93%	2e-60	UG			
XP_002372788.1	CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase [Arabidopsis thaliana] >dbj BAF2788.1 chitin elicitor receptor kinase 1 [Arabidopsis thaliana]	236	236	80%	8e-60	UG			
XP_002372788.1	unnamed protein product [Vitis vinifera]	234	234	95%	2e-50				
XP_002372788.1	PREDICTED: hypothetical protein [Vitis vinifera]	233	233	95%	4e-50	UG			

Alignments

Select All (6) Selected sequences Distance tree of results Multiple alignment

>gb ABQ59609.1 NFR5a [Glycine max]									
gb ADJ19105.1 G Nod-factor receptor 5A [Glycine max]									
gb ADJ19108.1 G Nod-factor receptor 5A [Glycine max]									
Length=598									
Score = 1235 bits (3196), Expect = 0.0, Method: Compositional matrix adjust.									
Identities = 598/598 (100%), Positives = 598/598 (100%), Gaps = 0/598 (0%)									
Query 1	MAVFPPFLPLHSQILCLVIMFLSTNIVAQSQDNRNFCPSDPSPCSCVTYVYIAQSPN	60							
Sbjct 1	MAVFPPFLPLHSQILCLVIMFLSTNIVAQSQDNRNFCPSDPSPCSCVTYVYIAQSPN	60							
Query 61	FLSLTNISNIFDTPSLTARSANLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ	120							
Sbjct 61	FLSLTNISNIFDTPSLTARSANLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ	120							
Query 121	QDSFYFVATTSYENLTNRWAVMDLNPVLSNPKLPIGIVVFLPCKCPKSNGLDKEIKYL	180							
Sbjct 121	QDSFYFVATTSYENLTNRWAVMDLNPVLSNPKLPIGIVVFLPCKCPKSNGLDKEIKYL	180							
Query 181	ITVVMKPGDNVLSVSKFGASPEDIMSENNYQGNFTAAANNLPVLPVTRPLVARSPSDG	240							
Sbjct 181	ITVVMKPGDNVLSVSKFGASPEDIMSENNYQGNFTAAANNLPVLPVTRPLVARSPSDG	240							
Query 241	RKGITRLPVITIGISGLCTLLVILAVLIVVYVCLMRKTINRSASSAETADKLLSGVSGYV	300							
Sbjct 241	RKGITRLPVITIGISGLCTLLVILAVLIVVYVCLMRKTINRSASSAETADKLLSGVSGYV	300							
Query 301	SKPTMYETDAIMEATMNLSECKI GSESVYKANIEGKVLAVRFKEDVTEELKILQKVNHG	360							
Sbjct 301	SKPTMYETDAIMEATMNLSECKI GSESVYKANIEGKVLAVRFKEDVTEELKILQKVNHG	360							
Query 361	NLWKMVGSDNDGNCFFVYVYEAENGSLDEWLFKSKCSDTNSRASLTWCQRISMAVDVA	420							
Sbjct 361	NLWKMVGSDNDGNCFFVYVYEAENGSLDEWLFKSKCSDTNSRASLTWCQRISMAVDVA	420							
Query 421	MGLQYMHAYPRIVRDTSSNILLDSNFKAIANTSMARTFTNMPMPKIDVFAFGVLL	480							
Sbjct 421	MGLQYMHAYPRIVRDTSSNILLDSNFKAIANTSMARTFTNMPMPKIDVFAFGVLL	480							
Query 481	IELLTGRKANTTKENGVEVMIMKDIKIFDQENREERLKKMMDPKLESYPIYDIALSLA	540							
Sbjct 481	IELLTGRKANTTKENGVEVMIMKDIKIFDQENREERLKKMMDPKLESYPIYDIALSLA	540							
Query 541	SLAVNCTADKSLSRPTIAEIVLSLSLTQSPATLERSITSSGLDVEATQVTSIAAR	598							
Sbjct 541	SLAVNCTADKSLSRPTIAEIVLSLSLTQSPATLERSITSSGLDVEATQVTSIAAR	598							

>gb ADJ19106.1 G Nod-factor receptor 5A [Glycine max]									
Length=598									
GENE ID: 10049858 NFR5a Nod-factor receptor 5A [Glycine max]									
(10 or fewer PubMed links)									
Score = 1233 bits (3189), Expect = 0.0, Method: Compositional matrix adjust.									
Identities = 597/598 (99%), Positives = 598/598 (100%), Gaps = 0/598 (0%)									
Query 1	MAVFPPFLPLHSQILCLVIMFLSTNIVAQSQDNRNFCPSDPSPCSCVTYVYIAQSPN	60							
	MAVFPPFLPLHSQILCLVIMFLSTNIVAQSQDNRNFCPSDPSPCSCVTYVYIAQSPN								

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Sbjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETVYTYIAQSPN 60
Query 61 FLSLTNISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
FLSLTINISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
Sbjct 61 FLSLTNISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
FLSLTINISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
Query 121 GDSFFVATTSYENLTNRWAVMDINPVLSPNKLPIGIVQVFLPCKCPKSNQLDKEIKYL 180
GDSFFVATTSYENLTNRWAVMDINPVLSPNKLPIGIVQVFLPCKCPKSNQLDKEIKYL 180
Sbjct 121 GDSFFVATTSYENLTNRWAVMDINPVLSPNKLPIGIVQVFLPCKCPKSNQLDKEIKYL 180
GDSFFVATTSYENLTNRWAVMDINPVLSPNKLPIGIVQVFLPCKCPKSNQLDKEIKYL 180
Query 181 ITTVWKGPDNVLSDSKFGASPEDIMSENNYQGNFTAAANLPLVLVPTLPLVARSFSDG 240
ITTVWKGPDNVLSDSKFGASPEDIMSENNYQGNFTAAANLPLVLVPTLPLVARSFSDG 240
Sbjct 181 ITTVWKGPDNVLSDSKFGASPEDIMSENNYQGNFTAAANLPLVLVPTLPLVARSFSDG 240
ITTVWKGPDNVLSDSKFGASPEDIMSENNYQGNFTAAANLPLVLVPTLPLVARSFSDG 240
Query 241 RKGGIRLPWIIIGISGLCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKILSGVSGV 300
RKGGIRLPWIIIGISGLCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKILSGVSGV 300
Sbjct 241 RKGGIRLPWIIIGISGLCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKILSGVSGV 300
RKGGIRLPWIIIGISGLCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKILSGVSGV 300
Query 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVRFKEDVTEELIKLQVNHG 360
SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVRFKEDVTEELIKLQVNHG 360
Sbjct 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVRFKEDVTEELIKLQVNHG 360
SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVRFKEDVTEELIKLQVNHG 360
Query 361 NLVKMGVSDNDGNCFFVYEAENGSLDEWLFBSKCSDTNSRASLTWCQRISMAVDVA 420
NLVKMGVSDNDGNCFFVYEAENGSLDEWLFBSKCSDTNSRASLTWCQRISMAVDVA 420
Sbjct 361 NLVKMGVSDNDGNCFFVYEAENGSLDEWLFBSKCSDTNSRASLTWCQRISMAVDVA 420
NLVKMGVSDNDGNCFFVYEAENGSLDEWLFBSKCSDTNSRASLTWCQRISMAVDVA 420
Query 421 MGLQYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL 480
MGLQYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL 480
Sbjct 421 MGLQYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL 480
MGLQYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL 480
Query 481 IELLTGKAKATKENGGEVVMWKDIWKIFDQENREERLKKMDPKLESYPIIDYALSIA 540
IELLTGKAKATKENGGEVVMWKDIWKIFDQENREERLKKMDPKLESYPIIDYALSIA 540
Sbjct 481 IELLTGKAKATKENGGEVVMWKDIWKIFDQENREERLKKMDPKLESYPIIDYALSIA 540
IELLTGKAKATKENGGEVVMWKDIWKIFDQENREERLKKMDPKLESYPIIDYALSIA 540
Query 541 SLAVNCTADKSLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSIAAR 598
SLAVNCTADKSLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSIAAR 598
Sbjct 541 SLAVNCTADKSLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSIAAR 598
SLAVNCTADKSLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSIAAR 598

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>gb|AD719107.1| [G] Nod-factor receptor 5A [Glycine max]
Length=598

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 1231 bits (3184), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 596/598 (99%), Positives = 598/598 (100%), Gaps = 0/598 (0%)

Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETVYTYIAQSPN 60
Sbjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETVYTYIAQSPN 60
Query 61 FLSLTNISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
FLSLTINISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
Sbjct 61 FLSLTNISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
FLSLTINISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
Query 121 GDSFFVATTSYENLTNRWAVMDINPVLSPNKLPIGIVQVFLPCKCPKSNQLDKEIKYL 180
GDSFFVATTSYENLTNRWAVMDINPVLSPNKLPIGIVQVFLPCKCPKSNQLDKEIKYL 180
Sbjct 121 GDSFFVATTSYENLTNRWAVMDINPVLSPNKLPIGIVQVFLPCKCPKSNQLDKEIKYL 180
GDSFFVATTSYENLTNRWAVMDINPVLSPNKLPIGIVQVFLPCKCPKSNQLDKEIKYL 180
Query 181 ITTVWKGPDNVLSDSKFGASPEDIMSENNYQGNFTAAANLPLVLVPTLPLVARSFSDG 240
ITTVWKGPDNVLSDSKFGASPEDIMSENNYQGNFTAAANLPLVLVPTLPLVARSFSDG 240
Sbjct 181 ITTVWKGPDNVLSDSKFGASPEDIMSENNYQGNFTAAANLPLVLVPTLPLVARSFSDG 240
ITTVWKGPDNVLSDSKFGASPEDIMSENNYQGNFTAAANLPLVLVPTLPLVARSFSDG 240
Query 241 RKGGIRLPWIIIGISGLCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKILSGVSGV 300
RKGGIRLPWIIIGISGLCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKILSGVSGV 300
Sbjct 241 RKGGIRLPWIIIGISGLCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKILSGVSGV 300
RKGGIRLPWIIIGISGLCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKILSGVSGV 300
Query 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVRFKEDVTEELIKLQVNHG 360
SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVRFKEDVTEELIKLQVNHG 360
Sbjct 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVRFKEDVTEELIKLQVNHG 360
SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVRFKEDVTEELIKLQVNHG 360
Query 361 NLVKMGVSDNDGNCFFVYEAENGSLDEWLFBSKCSDTNSRASLTWCQRISMAVDVA 420
NLVKMGVSDNDGNCFFVYEAENGSLDEWLFBSKCSDTNSRASLTWCQRISMAVDVA 420
Sbjct 361 NLVKMGVSDNDGNCFFVYEAENGSLDEWLFBSKCSDTNSRASLTWCQRISMAVDVA 420
NLVKMGVSDNDGNCFFVYEAENGSLDEWLFBSKCSDTNSRASLTWCQRISMAVDVA 420
Query 421 MGLQYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL 480
MGLQYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL 480
Sbjct 421 MGLQYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL 480
MGLQYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL 480
Query 481 IELLTGKAKATKENGGEVVMWKDIWKIFDQENREERLKKMDPKLESYPIIDYALSIA 540
IELLTGKAKATKENGGEVVMWKDIWKIFDQENREERLKKMDPKLESYPIIDYALSIA 540
Sbjct 481 IELLTGKAKATKENGGEVVMWKDIWKIFDQENREERLKKMDPKLESYPIIDYALSIA 540
IELLTGKAKATKENGGEVVMWKDIWKIFDQENREERLKKMDPKLESYPIIDYALSIA 540
Query 541 SLAVNCTADKSLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSIAAR 598
SLAVNCTADKSLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSIAAR 598
Sbjct 541 SLAVNCTADKSLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSIAAR 598
SLAVNCTADKSLSRPTIAEIVLSLITQSPATLERSITSSGLDVEATQVTSIAAR 598

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>gb|AD719112.1| [G] Nod-factor receptor 5B [Glycine max]
Length=599

GENE ID: 100498857 NFR5b | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score = 1106 bits (2861), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 563/599 (93%), Positives = 578/599 (96%), Gaps = 1/599 (0%)

Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETVYTYIAQSPN 59
MAVF FFL PL HSQ IL CL VIM LF ST NIVA QSQ Q DN RT NF SC PS DSP SC ET VY TY IA QSP N
Sbjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETVYTYIAQSPN 60
NFR5B:INISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ
Query 60 NFR5B:INISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 119
NFR5B:INISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
Sbjct 61 NFR5B:INISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
NFR5B:INISNIFDTSPSLIARASNLPEMDKILVDQVLLVPVTCGCTGNRSPANISYEINQ 120
Query 120 QDSFFVATTSYENLTNRWAVMDINPVLSPNKLPIGIVQVFLPCKCPKSNQLDKEIKYL 179

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Sbjct 121 GDSFYFVATTSSYENLTNRK VMDLNP LSPN LPIGIQVVPFLPCKPCPSKNQLDK IKY
PDSFYFVATTSSYENLTNRK VMDLNP LSPN LPIGIQVVPFLPCKPCPSKNQLDK IKY 180

Query 180 LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD
LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD 239

Sbjct 181 LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD
LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD 240

Query 240 GRKGIRLPLVITIGISLCTLLVLVLVAVLVVYVYCLMKMTINRSASSAETADKLLGVSQY
RGKIRLPLVITIGISLCTLLVLVLVAVLVVYVYCLMKMTINRSASSAETADKLLGVSQY 299

Sbjct 241 GRKGIRLPLVITIGISLCTLLVLVLVAVLVVYVYCLMKMTINRSASSAETADKLLGVSQY
RGKIRLPLVITIGISLCTLLVLVLVAVLVVYVYCLMKMTINRSASSAETADKLLGVSQY 300

Query 300 VSKPTMYETDAIMBATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELIKLQKVNH
VSKPTMYETDAIMBATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELIKLQKVNH 359

Sbjct 301 VSKPTMYETDAIMBATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELIKLQKVNH
VSKPTMYETDAIMBATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELIKLQKVNH 360

Query 360 GNVLKLMGVSDNDGNCFFVVEYAENGLDEWLFKSCSDTNSRASLTWCQRISMAVDV
GNVLKLMGVSDNDGNCFFVVEYAENGLDEWLFKSCSDTNSRASLTWCQRISMAVDV 419

Sbjct 361 GNVLKLMGVSDNDGNCFFVVEYAENGLDEWLFKSCSDTNSRASLTWCQRISMAVDV
GNVLKLMGVSDNDGNCFFVVEYAENGLDEWLFKSCSDTNSRASLTWCQRISMAVDV 420

Query 420 ANGQVMEHAYPRIVRHDITSSNLLDSNFKKAIANFSMARTFTNPMFKIDVFAFGVV
ANGQVMEHAYPRIVRHDITSSNLLDSNFKKAIANFSMARTFTNPMFKIDVFAFGVV 479

Sbjct 421 ANGQVMEHAYPRIVRHDITSSNLLDSNFKKAIANFSMARTFTNPMFKIDVFAFGVV
ANGQVMEHAYPRIVRHDITSSNLLDSNFKKAIANFSMARTFTNPMFKIDVFAFGVV 480

Query 480 LTELTLGRKAMTTKENGVEVMLMKDVKIFDQENREERLAKKMDPKLESYYPIDYALS
LTELTLGRKAMTTKENGVEVMLMKDVKIFDQENREERLAKKMDPKLESYYPIDYALS 539

Sbjct 481 LTELTLGRKAMTTKENGVEVMLMKDVKIFDQENREERLAKKMDPKLESYYPIDYALS
LTELTLGRKAMTTKENGVEVMLMKDVKIFDQENREERLAKKMDPKLESYYPIDYALS 540

Query 540 ASLAVNCTADKLSRPTTAEIVLSILITQPSPATLERSLTSSGLDVEATQIVTSIAAR
ASLAVNCTADKLSRPTTAEIVLSILITQPSPATLERSLTSSGLDVEATQIVTSIAAR 598

Sbjct 541 ASLAVNCTADKLSRPTTAEIVLSILITQPSPATLERSLTSSGLDVEATQIVTSIAAR
ASLAVNCTADKLSRPTTAEIVLSILITQPSPATLERSLTSSGLDVEATQIVTSIAAR 599

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>gb|ADJ19111.1|  Nod-factor receptor 5B [Glycine max]

Length=599

GENE ID: 100498857 WFR5b | Nod-factor receptor 5B [Glycine max]

(10 or fewer PubMed links)

Score = 1103 bits (2854), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 562/599 (93%), Positives = 577/599 (96%), Gaps = 1/599 (0%)

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Query 1 MAVFPPFLPLASQILCLVIMLFSTNIVAQSQQDNRNFCSPDSPSPSC-ETTVYIAQSP 59
MAVF FFLPLASQILCLVIMLFSTNIVAQSQQDNRNFCSPDSPSPSC-ETTVYIAQSP 60
Sbjct 1 MAVFPPFLPLASQILCLVIMLFSTNIVAQSQQDNRNFCSPDSPSPSC-ETTVYIAQSP 59
MAVFPPFLPLASQILCLVIMLFSTNIVAQSQQDNRNFCSPDSPSPSC-ETTVYIAQSP 60

Query 60 NPLSTNIGSINIFTDPSLARSANLEPMDDKLVQDVLVLPVTCGCTGNRSFANISYEIN
NPLSTNIGSINIFTDPSLARSANLEPMDDKLVQDVLVLPVTCGCTGNRSFANISYEIN 119
Sbjct 61 NPLSTNIGSINIFTDPSLARSANLEPMDDKLVQDVLVLPVTCGCTGNRSFANISYEIN
NPLSTNIGSINIFTDPSLARSANLEPMDDKLVQDVLVLPVTCGCTGNRSFANISYEIN 120

Query 120 GDSFYFVATTSSYENLTNRK VMDLNP LSPN LPIGIQVVPFLPCKPCPSKNQLDK IKY
PDSFYFVATTSSYENLTNRK VMDLNP LSPN LPIGIQVVPFLPCKPCPSKNQLDK IKY 179

Sbjct 121 GDSFYFVATTSSYENLTNRK VMDLNP LSPN LPIGIQVVPFLPCKPCPSKNQLDK IKY
PDSFYFVATTSSYENLTNRK VMDLNP LSPN LPIGIQVVPFLPCKPCPSKNQLDK IKY 180

Query 180 LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD
LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD 239

Sbjct 181 LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD
LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD 240

Query 240 GRKGIRLPLVITIGISLCTLLVLVLVAVLVVYVYCLMKMTINRSASSAETADKLLGVSQY
RGKIRLPLVITIGISLCTLLVLVLVAVLVVYVYCLMKMTINRSASSAETADKLLGVSQY 299

Sbjct 241 GRKGIRLPLVITIGISLCTLLVLVLVAVLVVYVYCLMKMTINRSASSAETADKLLGVSQY
RGKIRLPLVITIGISLCTLLVLVLVAVLVVYVYCLMKMTINRSASSAETADKLLGVSQY 300

Query 300 VSKPTMYETDAIMBATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELIKLQKVNH
VSKPTMYETDAIMBATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELIKLQKVNH 359

Sbjct 301 VSKPTMYETDAIMBATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELIKLQKVNH
VSKPTMYETDAIMBATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELIKLQKVNH 360

Query 360 GNVLKLMGVSDNDGNCFFVVEYAENGLDEWLFKSCSDTNSRASLTWCQRISMAVDV
GNVLKLMGVSDNDGNCFFVVEYAENGLDEWLFKSCSDTNSRASLTWCQRISMAVDV 419

Sbjct 361 GNVLKLMGVSDNDGNCFFVVEYAENGLDEWLFKSCSDTNSRASLTWCQRISMAVDV
GNVLKLMGVSDNDGNCFFVVEYAENGLDEWLFKSCSDTNSRASLTWCQRISMAVDV 420

Query 420 ANGQVMEHAYPRIVRHDITSSNLLDSNFKKAIANFSMARTFTNPMFKIDVFAFGVV
ANGQVMEHAYPRIVRHDITSSNLLDSNFKKAIANFSMARTFTNPMFKIDVFAFGVV 479

Sbjct 421 ANGQVMEHAYPRIVRHDITSSNLLDSNFKKAIANFSMARTFTNPMFKIDVFAFGVV
ANGQVMEHAYPRIVRHDITSSNLLDSNFKKAIANFSMARTFTNPMFKIDVFAFGVV 480


Query 480 LTELTLGRKAMTTKENGVEVMLMKDVKIFDQENREERLAKKMDPKLESYYPIDYALS
LTELTLGRKAMTTKENGVEVMLMKDVKIFDQENREERLAKKMDPKLESYYPIDYALS 539

Sbjct 481 LTELTLGRKAMTTKENGVEVMLMKDVKIFDQENREERLAKKMDPKLESYYPIDYALS
LTELTLGRKAMTTKENGVEVMLMKDVKIFDQENREERLAKKMDPKLESYYPIDYALS 540

Query 540 ASLAVNCTADKLSRPTTAEIVLSILITQPSPATLERSLTSSGLDVEATQIVTSIAAR
ASLAVNCTADKLSRPTTAEIVLSILITQPSPATLERSLTSSGLDVEATQIVTSIAAR 598

Sbjct 541 ASLAVNCTADKLSRPTTAEIVLSILITQPSPATLERSLTSSGLDVEATQIVTSIAAR
ASLAVNCTADKLSRPTTAEIVLSILITQPSPATLERSLTSSGLDVEATQIVTSIAAR 599

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>gb|ADJ19110.1|  truncated Nod-factor receptor 5A [Glycine max]

Length=501

GENE ID: 100498858 WFR5a | Nod-factor receptor 5A [Glycine max]

(10 or fewer PubMed links)

Score = 1037 bits (2682), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 501/501 (100%), Positives = 501/501 (100%), Gaps = 0/501 (0%)

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Query 1 MAVFPPFLPLASQILCLVIMLFSTNIVAQSQQDNRNFCSPDSPSPSC-ETTVYIAQSP 60
MAVFPPFLPLASQILCLVIMLFSTNIVAQSQQDNRNFCSPDSPSPSC-ETTVYIAQSP 60
Sbjct 1 MAVFPPFLPLASQILCLVIMLFSTNIVAQSQQDNRNFCSPDSPSPSC-ETTVYIAQSP 60
MAVFPPFLPLASQILCLVIMLFSTNIVAQSQQDNRNFCSPDSPSPSC-ETTVYIAQSP 60

Query 61 FLSTNIGSINIFTDPSLARSANLEPMDDKLVQDVLVLPVTCGCTGNRSFANISYEINQ
FLSTNIGSINIFTDPSLARSANLEPMDDKLVQDVLVLPVTCGCTGNRSFANISYEINQ 120
Sbjct 61 FLSTNIGSINIFTDPSLARSANLEPMDDKLVQDVLVLPVTCGCTGNRSFANISYEINQ
FLSTNIGSINIFTDPSLARSANLEPMDDKLVQDVLVLPVTCGCTGNRSFANISYEINQ 120

Query 121 GDSFYFVATTSSYENLTNRK VMDLNP LSPN LPIGIQVVPFLPCKPCPSKNQLDK IKY
PDSFYFVATTSSYENLTNRK VMDLNP LSPN LPIGIQVVPFLPCKPCPSKNQLDK IKY 180

Sbjct 121 GDSFYFVATTSSYENLTNRK VMDLNP LSPN LPIGIQVVPFLPCKPCPSKNQLDK IKY
PDSFYFVATTSSYENLTNRK VMDLNP LSPN LPIGIQVVPFLPCKPCPSKNQLDK IKY 180

Query 181 LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD
LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD 240

Sbjct 181 LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD
LITVYWKPGDNVSLVSDKFGASPEDIMSENNYGNFTAAANLVLVLPVTRLVPLARSPPD 240

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Query 241 RKGGIRLPLVIGISLGLTLLVLVLAVLIVVYVCLMKMTINRSASSAETADKLLSGVSGVY 300
Sbjct 241 RKGGIRLPLVIGISLGLTLLVLVLAVLIVVYVCLMKMTINRSASSAETADKLLSGVSGVY 300

Query 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELIKLQVNHG 360
Sbjct 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELIKLQVNHG 360

Query 361 NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFPSKSCSDTNSRASLTWCQRISMADVVA 420
Sbjct 361 NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFPSKSCSDTNSRASLTWCQRISMADVVA 420

Query 421 MGQYMHIEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL 480
Sbjct 421 MGQYMHIEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL 480

Query 481 IELLTGKAKMTTKNGEVMVL 501
Sbjct 481 IELLTGKAKMTTKNGEVMVL 501

>gb|AB059613.1| NFR5B [Glycine max]
Length=515

Score = 957 bits (2475), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 478/504 (94%), Positives = 491/504 (97%), Gaps = 0/504 (0%)

Query 95 QVLLPVTGCTGNRSFANIYEINQGDSPFYVATTSYENLNNHVAAMDINPVLSPNKL 154
Sbjct 12 QVLLPVTGCTGNRSFANIYEINQGDSPFYVATTSYENLNNHVAAMDINPVLSPNKL 71

Query 155 IQGVVFLPCKCPKSNGLDKIKYLLITYVWQPNVLSLVSEKFGASPEDIISENNGCN 214
Sbjct 72 IQGVVFLPCKCPKSNGLDKIKYLLITYVWQPNVLSLVSEKFGASPEDIISENNGCN 131

Query 215 FTAANNLPVLIPVTRLEPLARSPSDRKGIRLPLVIGISLGLTLLVLVLAVLIVVYCL 174
Sbjct 132 FTAANNLPVLIPVTRLEPLVIA+ PSD RKGGIRLPLVIGISLGLTLLVLVLAVLIVVYCL 294

Query 275 NKMTINRSASSAETADKLLSGVSGVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIE 334
Sbjct 192 K+K+LNDIMEATMNLSE+CKIGESVYKANIE
KIS+NRSSASSAETADKLLSGVSGVSKPTMYETDAIMEATMNLSECKIGESVYKANIE 251

Query 335 GKVLAVKRFKEDVTEELIKLQVNHGILVKIMGVSSDNDGNCFFVVEYAENGSLDEWLF 394
Sbjct 252 GKVLAVKRFKEDVTEELIKLQVNHGILVKIMGVSSDNDGNCFFVVEYAENGSLDEWLF 311

Query 395 KSCSDTNSRASLTWCQRISMADVAMGLQYMHIEHAYPRIVHRDITSSNILLDSNFKAKI 454
Sbjct 312 KSCSDTNSRASLTWCQRIS+AVDAMGLQYMHIEHAYPRIVHRDITSSNILLDSNFKAKI 371

Query 455 ANFSMARTFTNPMMPKIDVFAFGVVLIELLTGKAKMTTKNGEVMVLAKMDIKWIFDQEN 514
Sbjct 372 ANFSMARTFTNPMMPKIDVFAFGVVLIELLTGKAKMTTKNGEVMVLAKMDIKWIFDQEN 431

Query 515 REERLKKWMDPKLESYYPIDYALSASLAVNCTADKLSRSTIAEIVLSISLITQPSFAT 574
Sbjct 432 REERLKKWMDPKLESYYPIDYALSASLAVNCTADKLSRSTIAEIVLSISLITQPSFAT 491

Query 575 IERSLTSBGLDVEATQVITSIAAR 598
Sbjct 492 IERSLTSBGLDVEATQVITSIAAR 515

>emb|CAE02593.1| SYM10 protein [Pisum sativum]
>emb|CAE02594.1| SYM10 protein [Pisum sativum]
Length=594

Score = 899 bits (2322), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 451/600 (75%), Positives = 505/600 (84%), Gaps = 0/600 (1%)

Query 1 MAVTFPFLELSQSGLCLVIMLFSTNIVAQSGQDRNTNFCSPDSFSPSCETVYVTAQSPN 60
Sbjct 1 MAVTF--LPSSSHALFLALMFVFNISAQPLQLSGTNFCSPDFSPSCETVYVTAQSPN 58

Query 61 FLSTNTNISIFDTPSLSTARASNLPEWDDKLVKDQVLLVPVTCGCTGNRSFANIYEINQ 120
Sbjct 59 FLSTNTNIS+IFD SPLSTA+ASN+E D KLV+ QVLL+PVTGCTGR N FAN +Y I
FLSTNTNISIDFMDPSLSTARASNIEDEDDKLVQEGQVLLVPVTCGCTGRNRYFANFTYIKL 118

Query 121 GDSFFVATTSYENLNNHVAAMDINPVLSPNKLPIQGVVFLPCKCPKSNGLDKIKYLL 180
Sbjct 119 GDSFFVATTSYENLNNHVAAMDINPVLSPNKLPIQGVVFLPCKCPKSNGLDKIKYLL 178

Query 181 ITVYVWQPNVLSLVSEKFGASPEDIISENNGCNQFTANNLPVLIPVTRLEPLARSPSDG 240
Sbjct 179 ITVYVWQPNVLSLVSEKFGASPEDIISENNGCNQFTANNLPVLIPVTRLEPLARSPSDG 236

Query 241 RKGGIRLPLVIGISLGLTLLVLVLAVLIVVYVCLMKMTINRSASSAETADKLLSGVSGY 299
Sbjct 237 RK+ +P IIGISLGC V+VL +LVVYVCLMK INRS S AETADKLLSGVSGY 296

Query 300 VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELIKLQVNH 359
Sbjct 297 VSKPTMYETDAIMEATMNLSECKIGESVYKANIEGKVLAVKRFKEDVTEELIKLQVNH 356

Query 360 NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFESKSCSDTNSRASLTWCQRISMADV 419
Sbjct 357 NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFESKSCSDTNSRASLTWCQRISMADV 415

Query 420 AMGLQYMHIEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGV 475
Sbjct 416 AMGLQYMHIEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGV 475

Query 480 IELLTGKAKMTTKNGEVMVLAKMDIKWIFDQENREERLKKWMDPKLESYYPIDYALS 539
Sbjct 476 IELLTGKAKMTTKNGEVMVLAKMDIKWIFDQENREERLKKWMDPKLESYYPIDYALS 535

Query 540 ASLAVNCTADKLSRSTIAEIVLSISLITQPSFA--TLERSLTSBGLDVEATQVITSIAAR 598

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ASLAVNCTADKSLSRP+TAEIVL LSLI Q S LERSIT SGLDVEAT +VTSI AR
 Sbjct 536 ASLAVNCTADKSLSRPSTAEIVLCLISLILNQSSEPMLESLT-SGLDVEATHVVTISVAR 594

>emb|CAK02595.1| SYM10 protein [Pisum sativum]
 emb|CAK02596.1| SYM10 protein [Pisum sativum]
 gb|AB045277.1| Nod factor recognition protein [Pisum sativum]
 Length=594

Score = 895 bits (2312), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 449/600 (74%), Positives = 504/600 (84%), Gaps = 8/600 (1%)

Query 1 MAVFFPPLFLHSQILCLVIMLFSTNIQAQSDNRTNFCPSDPPSCETVYTYIAQSPN 60
 MAVFF LP S L L +M F TNI AQ Q + TNPSC DPSPSCETVYTY +SPN
 Sbjct 1 MAVFF--LPSSSHALFLAMFVTWNISAQPLQSGTNFCPSDFDPPSCETVYTYIAQSPN 58

Query 61 FLSTNLSINISDTPSLSTARASNLPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQ 120
 FLSTNLS+IED SPSTASRAN+E D KLV+ QVLLVPVTCG GR S AN SY+I
 Sbjct 59 FLSTNLSIDTPDPSLSTARASNLIEDKLVQVLLVPVTCGCTGNRSFANISYEIKL 118

Query 121 GDSYFVATTSEYENLNWRAMVDLPVLPSPKRLPICIQVVPFLCPCKPSNGLDKEIKYL 180
 GD++ V+TTRY+NLN+ + + NP LSPN LP +VV PLCPCKPSNGL K+K+L
 Sbjct 119 GDNFYFVSTSYQNLNTYEMENFNPNLSNPLLPPIKVVVPLCPCKPSNGLSKGSKHL 178

Query 181 ITTVWKPQDNVSLVSKFGASPEDIMENNYQNFTAAANLVLPIVTLPLVARSFSDG 240
 ITTVW+ DN+ VS KFGAS D+ ENN QNTA+ N+P+L+PVT+LP+ + S+G
 Sbjct 179 ITTVWKNQNVTVSKFGASQVWMTENN--QNPASTNVLPIVTLPLVTLQPSMG 236

Query 241 RKGITLRFVPIIGISLGLTLLVLAVLVLVYVCLMKNTLRNASSAETADKLLSGVSGY 299
 K+ P + IIGISLGC +VVI+ LVYVYCLMKK INN S AETADKLLSGVSGY
 Sbjct 237 RKNSTKAPFIIGISLGCAPFVVLITSLVYVCLMKRLNRSTLSAETADKLLSGVSGY 296

Query 300 VSKPTMYEIDAIMEATMNLSEQCKIGESVYKANIEGVLAVRKFEDVTEELKILQKVNH 359
 VSKPTMYE DAIMEATMNLSE CRIGESVYKANIG+VLAVK+ K+D +EELKILQKVNH
 Sbjct 297 VSKPTMYEIDAIMEATMNLSENCKIGESVYKANIDGRVLAVRKIKDASEELKILQKVNH 356

Query 360 GNVLKMGVSDNDGNCFFVVEYAENGSLDEWLFPSKSCSDTNSNRASLTWCORISMAVDV 419
 GNVLKMGVSDNDGNCFFVVEYAENGSLDEWLF+ S TNS+ SLTA GR+I+AVDV
 Sbjct 357 GNVLKMGVSDNDGNCFLVVEYAENGSLDEWLFSE--LSKTSNSVSLTWCGRITVAVDV 415

Query 420 ANGLQYMHSHAYPRIVHRTDTSNILLDSNFKAIANFSMARTTNPMPKIDVFAFGVV 479
 A+GLQYMHSH YPRI+HRDI+TSNILLDSNFKAIANFSMART TN MPKIDVFAFGVV
 Sbjct 416 AVGLQYMHSHETPRIHRDITTSNILLDSNFKAIANFSMARTSTNSMPKIDVFAFGVV 475

Query 480 LIETLLGRKAMTTKENGVEVMMLKMDIKWIFDQENREERLKKWMDPKLESYYPIDYALS 539
 LIETLLGRKAMTTKENGVEVMMLKMD+H+IFD ENREER++KMDPKLE+YID ALSL
 Sbjct 476 LIETLLGRKAMTTKENGVEVMMLKMDIKWIFDQENREERLKKWMDPKLENYPIIDNALS 535

Query 540 ASLAVNCTADKSLSRPTAEIVLSLISLTQPSA+TLERSITSGLDVEATQIVTSTAAR 598
 ASLAVNCTADKSLSRP+TAEIVL LSLI Q S LERSIT SGLDVEAT +VTSI AR
 Sbjct 536 ASLAVNCTADKSLSRPTAEIVLCLISLILNQSSEPMLESLT-SGLDVEATHVVTISVAR 594

>emb|CAK02597.1| G Nod-factor receptor 5 [Lotus japonicus]
 emb|CAK02598.1| G Nod-factor receptor 5 [Lotus japonicus]
 Length=595

GENE ID: 100034751 NFR5 | Nod-factor receptor 5 [Lotus japonicus]
 (10 or fewer PubMed links)

Score = 875 bits (2262), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 449/601 (74%), Positives = 500/601 (83%), Gaps = 9/601 (1%)

Query 1 MAVFFPPLFLHSQILCLVIMLFSTNIQAQSDNRTNFCPSDPPSCETVYTYIAQSPN 60
 MAVFF L S L L +L TNI A+S++ +FSCP DPSPSCETVYTY AQSPN
 Sbjct 1 MAVFF--LTSGSLSLFLALTLFTNTAARSEKISGDFPCPSDFDPPSCETVYTYIAQSPN 58

Query 61 FLSTNLSINISDTPSLSTARASNLPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQ 120
 FLSTNLS+IED SPSTASRAN++ D KLV QVLLVPVTCG CG GR S AN SY+I
 Sbjct 59 FLSTNLSIDTPDPSLSTARASNLDAKQKLVQVLLVPVTCGCTGNRSFANISYIQIL 118

Query 121 GDSYFVATTSEYENLNWRAMVDLPVLPSPKRLPICIQVVPFLCPCKPSNGLDKEIKYL 180
 GD+ FVATT YENLNW V NP +P LP +VVVPLFC+CPSPNGL K+Y+L
 Sbjct 119 GDSYFVATTIYENLTWNINVAQSNPQVNPYLLPERVKVVPFLCPCKPSNGLNKGQYVL 178

Query 181 ITTVWKPQDNVSLVSKFGASPEDIMENNYQNFTAAANLVLPIVTLPLVARSFSDG 240
 ITTVWKP QDNVSLV KFGASP DI+EN YQ+PTAA NL+L+PVT+LP L + S+G
 Sbjct 179 ITTVWKNQDNVSLVSKFGASPADILFENRYGQDTAATNLPIFLVTLQPSMG 238

Query 241 RKGITLRFVPIIGISLGLTLLVLAVLVLVYVCLMKNTLRNASSAETADKLLSGVSGY 299
 R+ P + IIGISLGLTLLVAVLVLVYVCLMKK INN S AETADKLLSGVSGY
 Sbjct 239 RKSSITLVLIGITLGLTLLVAVLGLVYVCRKKAIRNATSSAETADKLLSGVSGY 298

Query 301 SKPTMYEIDAIMEATMNLSEQCKIGESVYKANIEGVLAVRKFEDVTEELKILQKVNH 359
 SKP +YE D IMEAT + S+CK+GESVYKANIEG+V+AVK+ KE EELKILQKVNH
 Sbjct 299 SKPNVYIDEIMEATKPSDECKVGEVYKANIEGRVAVVKKIKEGGANEELKILQKVNH 358

Query 360 GNVLKMGVSDNDGNCFFVVEYAENGSLDEWLFPSKSCSDTNSNRASLTWCORISMAVDV 419
 GNVLKMGVSDNDGNCFFVVEYAENGSLDEWLFPSKSCSDTNSNRASLTWCORISMAVDV
 Sbjct 359 GNVLKMGVSDNDGNCFLVVEYAENGSLDEWLFPSKSCSDTNSNRASLTWCORISMAVDV 414

Query 420 ANGLQYMHSHAYPRIVHRTDTSNILLDSNFKAIANFSMARTTNPMPKIDVFAFGVV 479
 A+GLQYMHSH YPRI+HRDI+TSNILLDSNFKAIANF+MART TNPMPKIDVFAFGVV
 Sbjct 415 AVGLQYMHSHETPRIHRDITTSNILLDSNFKAIANFAMARTSTNMPKIDVFAFGVV 474

Query 480 LIETLLGRKAMTTKENGVEVMMLKMDIKWIFDQENREERLKKWMDPKLESYYPIDYALS 539
 LIETLLGRKAMTTKENGVEVMMLKMD+H+IFD ENREER++KMDPKLE+YID ALSL
 Sbjct 475 LIETLLGRKAMTTKENGVEVMMLKMDIKWIFDQENREERLKKWMDPKLESYYPIDYALS 534

Query 540 ASLAVNCTADKSLSRPTAEIVLSLISLTQPSA+TLERSITSGLDVEATQIVTSTAAR 597
 ASLAVNCTADKSLSRP+TAEIVL LSLI Q S LERSIT SGLDVEAT +VTSI AR
 Sbjct 535 ASLAVNCTADKSLSRPMAEIVLSLISLTQPS+TLERSITSGLDVEADHIVTSTPA 594

Query 598 R 598
 Sbjct 595 R 595

>gb|ABF50224.1| Nod factor perception protein [Medicago truncatula]
Length=595

Score = 864 bits (2232), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 429/577 (74%), Positives = 485/577 (84%), Gaps = 6/577 (1%)

Query 24 TNVAQSQQDNTRNFCPSPPSPSCETVYVYIAQSPNPLSITNSINIDTSSLIARASN 83
TNI AQ + NPFCPSPPSCETVY V AQSFPNPLSINIS+IF+ SPL IA+ASN+ D KI+ DQ+LLVPTGCG
Sbjct 23 TNISQPLIYBETNFCPSPPSCETVYVYIAQSPNPLSINISINIDTSSLIARASN 82

Query 84 LEPMDDKLKQDVLLVPTGCGCTKNSRSPANITYSIKQGNFFLISITSYQNLTYLEFRN 143
+E D KL+ DQ+LLVPTGCGT N SFANI+Y I QCD+P+ ++ TSY+NLTN+
Sbjct 83 LEARDKKLI PQDLLVPTGCGCTKNSRSPANITYSIKQGNFFLISITSYQNLTYLEFRN 142

Query 144 INPVLSPNKLPIGIGVVFPLFCPCPSKNQDKKEIKYLYTVKPGDNVLSVSKFGASPE 203
NP LSP LP+ +V PLFCPCPSKNQ+K IKYLYTVVM+ DNV+LVS KFGAS
Sbjct 143 INPVLSPNKLPIGIGVVFPLFCPCPSKNQDKKEIKYLYTVKPGDNVLSVSKFGASGV 202

Query 204 DIMSENKYNQNTAANNLPVLIPTVRLPVLARSPSDGRGGIR+LPVIGISIGCTLLVL 262
+L NI+GRK +P L +S+GRK +L +I+IGISIG +LVL +LVVYVCLMRK LNRS 260
Sbjct 203 EMIAENNH--NFTASTNRSLVLPVTLSPKLPQPSNCRKSSSINALLIGISIGSAFFLI 261

Query 263 VLAIVLVVYVCLMRKLNRSASSAETADKLLSGVSGVSKPTMYETAIMEATMNLSEOC 322
VL+ LVVYVCLMRK LNRS SS+ETADKLLSGVSGVSKPTMYE DAIME T NLS+ C
Sbjct 261 VLTLLSVVYVCLMRKLNRSSTSSSETADKLLSGVSGVSKPTMYETAIMEATMNLSDNC 320

Query 323 KIGSVYKANI+G+VLAVER+K+D +EELKILQVNHGNLVKMGVSSDNDGNCFFVVEY 382
KIGSVYKANI+G+VLAVER+K+D +EELKILQVNHGNLVKMGVSSDNDGNCFFVVEY
Sbjct 321 KIGSVYKANI+G+VLAVER+K+D +EELKILQVNHGNLVKMGVSSDNDGNCFFVVEY 380

Query 383 AENGSLDEWLFKSSCDTNSRSL+TCKRIEMAVDVMGLQVMEHAYPRIVHRDITSS 442
AENGSLDEWLFKSS+STNS SLW QRI+ADVA+GLQVMEH YPRIVHRDITSS
Sbjct 381 AENGSLDEWLFKSS+STNSRSL+TCKRIEMAVDVMGLQVMEHAYPRIVHRDITSS 439

Query 443 NILLDSNFKAKIANFSMARTPTNPMKPIDVFAFGVLIILLTGKAMTTKENGVEVVLW 502
NILL SNFKAKIANF MART TN MMKPIDVFAFGVLIILLTG+KAMTTKENGVEVVLW
Sbjct 440 NILLDSNFKAKIANFSMARTPTNPMKPIDVFAFGVLIILLTGKAMTTKENGVEVVLW 499

Query 503 KDWKIFDQENREERLKKWMDPKLESYPIDVALSIASLAVNCTADKLSRPRTIATIVL 566
KDWKIFDQENREERLKKWMDPKLES+YPI D ALSIASLAVNCTADKLSRPRTIATIVL
Sbjct 500 KDWKIFDQENREERLKKWMDPKLESYPIDVALSIASLAVNCTADKLSRPRTIATIVL 559

Query 563 SLGLTQPSBA+TLERSLTSSGLDVEATQIVTSIAR 598
LGLT QPS LERSLT SGLD EAT +VTS+ AR
Sbjct 560 CLSLNGPSSPMLERSLT-SGLDAETHVTVSIAR 595

>emb|CAO02956.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
var. truncatula
Length=498

Score = 761 bits (1966), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 370/497 (74%), Positives = 423/497 (85%), Gaps = 4/497 (0%)

Query 46 PSCEITYVYIAQSPNPLSITNSINIDTSSLIARASNLEPMDDKLKQDVLLVPTGCG 105
PSCEITYV Y AQSFPNPLSINIS+IF+ SPL IA+ASN+ D KI+ DQ+LLVPTGCG
Sbjct 4 PSCEITYVATQAQSPNPLSINISINIDTSSLIARASNLEAEDKKLI PQDLLVPTGCG 63

Query 106 TGNRSPANITYSIKQGNFFLISITSYQNLTYLEFRNPNPVLSPNKLPIGIGVVFPLFC 125
+N SFANI+Y I QCD+P+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFC
Sbjct 64 TKNRSPANITYSIKQGNFFLISITSYQNLTYLEFRNPNPVLSPNKLPIGIGVVFPLFC 123

Query 166 KCPKSNQDKKEIKYLYTVKPGDNVLSVSKFGASPEDIMSENKYNQNTAANNLPVLI 225
KCPKSNQDK+K IKYLYTVVM+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLI
Sbjct 124 KCPKSNQDKKEIKYLYTVKPGDNVLSVSKFGASQVEMIAENNH--NFTASTNRSLVLI 181

Query 226 VPTVRLPVLARSPSDGRGGIR+LPVIGISIGCTLLVLVLAIVLVVYVCLMRKLNRS 284
PVT LP L +S+GRK +L +I+IGISIG +LVL +LVVYVCLMRK LNRS 281
Sbjct 182 VPTVRLPVLARSPSDGRGGIR+LPVIGISIGCTLLVLVLAIVLVVYVCLMRKLNRS 241

Query 285 SAETADKLLSGVSGVSKPTMYETAIMEATMNLSEOCKEIGSVYKANI+GKGLVLAVERK 344
SAETADKLLSGVSGVSKPTMYE DAIME TNNLS+ CRIGSVYKANI+G+VLAVER+ K
Sbjct 242 SAETADKLLSGVSGVSKPTMYETAIMEATMNLSDNCKEIGSVYKANI+GKGLVLAVERK 301

Query 345 EDVTEELKILQVNHGNLVKMGVSSDNDGNCFFVVEYAEENGSLDEWLFKSSCDTNSR 404
+D +EELKILQVNHGNLVKMGVSSDNDGNCFFVVEYAEENGSL+EWLF+8+STNS
Sbjct 302 KDAEELKILQVNHGNLVKMGVSSDNDGNCFFVVEYAEENGSLDEWLFKSS+STNSNV 400

Query 405 ASLWTCQRIEMAVDVMGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTPT 464
SLW QRI+ADVA+GLQVMEH YPRIVHRDITSSNILL SNFKAKIANF MART T
Sbjct 361 VSLWTCQRIEMAVDVMGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTPT 420

Query 465 NNMKPIDVFAFGVLIILLTG+KAMTTKENGVEVVLWMD KWFID E NREERL+K+K+MD 524
N NMKPIDVFAFGVLIILLTG+KAMTTKENGVEVVLWMD KWFID E NREERL+K+K+MD
Sbjct 421 NNMKPIDVFAFGVLIILLTG+KAMTTKENGVEVVLWMD KWFID E NREERL+K+K+MD 480

Query 525 PKLESYPIDVALSIAS 541
PKLES+YPI D ALS+AS
Sbjct 481 PKLESYPIDVALSIAS 497

>emb|CAO02958.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
var. truncatula
Length=492

Score = 754 bits (1948), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 367/494 (74%), Positives = 420/494 (85%), Gaps = 4/494 (0%)

Query 49 ETVVYVYIAQSPNPLSITNSINIDTSSLIARASNLEPMDDKLKQDVLLVPTGCGTGN 108
ETVVY V AQSFPNPLSINIS+IF+ SPL IA+ASN+ D KI+ DQ+LLVPTGCGT N
Sbjct 1 ETVVYVYIAQSPNPLSINISINIDTSSLIARASNLEAEDKKLI PQDLLVPTGCGTGN 60

Query 109 RSPANITYSIKQGNFFLISITSYQNLTYLEFRNPNPVLSPNKLPIGIGVVFPLFCPC 168
SPANIT+Y I QCD+P+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCPC
Sbjct 61 RSPANITYSIKQGNFFLISITSYQNLTYLEFRNPNPVLSPNKLPIGIGVVFPLFCPC 120

Query 169 SKNQDKKEIKYLYTVKPGDNVLSVSKFGASPEDIMSENKYNQNTAANNLPVLIPTV 228

Sbjct 121 SKNQI+K IKYLITYVM+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIPVT 178
SKNQI+KGIKYLITYVMQDNNDVTVSSKFGASQVEMLAENH--NFTASTNRSVLIPVT

Query 229 LPLVARSQDGRKGIR-LPVIIGISLGCTLLVLVLAVLIVVYCLMKTLNRSASSAE 287
LP L + 8+GRK + L +IIGISLG +IVL + LVVYCLMK LNRS SS+E

Sbjct 179 SLPKLDQSPNSGRKSSQNLALIGISLGSFAFLLVLTLSLVVYCLMKLNRSSTSE 238
SLPKLDQSPNSGRKSSQNLALIGISLGSFAFLLVLTLSLVVYCLMKLNRSSTSE

Query 288 TADKLLSGVSGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIGKVLAVKRFKEDV 347
TADKLLSGVSGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIGKVLAVKRFKEDV

Sbjct 239 TADKLLSGVSGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIGKVLAVKRFKEDV 298
TADKLLSGVSGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIGKVLAVKRFKEDV

Query 348 TEELKILQKVNHNKLMVSSDNDGNCVFVYEAENGSLDEWLFPSKSDTNSRSLTWOOR 407
TEELKILQKVNHNKLMVSSDNDGNCVFVYEAENGSLDEWLFPSKSDTNSRSLTWOOR

Sbjct 299 SEELKILQKVNHNKLMVSSDNDGNCVFVYEAENGSLDEWLFPSKSDTNSRSLTWOOR 357
SEELKILQKVNHNKLMVSSDNDGNCVFVYEAENGSLDEWLFPSKSDTNSRSLTWOOR

Query 408 TWQCRISMAVDVAMGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNM 467
TW QRI++A+DVA+GLQVMEH YPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNM

Sbjct 358 TWQRI++A+DVA+GLQVMEH YPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNM 417
TWQRI++A+DVA+GLQVMEH YPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNM

Query 468 MPKIDVAFGVLLITGKAMTTKENGVEVVLKMDKFIQDQENREERLRKMMDPKLL 527
MPKIDVAFGVLLITGKAMTTKENGVEVVLKMDKFIQDQENREERLRKMMDPKLL

Sbjct 418 MPKIDVAFGVLLITGKAMTTKENGVEVVLKMDKFIQDQENREERLRKMMDPKLL 477
MPKIDVAFGVLLITGKAMTTKENGVEVVLKMDKFIQDQENREERLRKMMDPKLL

Query 528 ESYYPIDYALSLAS 541
ES+YPD ALS+AS

Sbjct 478 ESYYPIDNALSMAS 491
ESYPIDNALSMAS

>emb|CA002933.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002934.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002935.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
10 more sequence titles
emb|CA002938.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002939.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002952.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. longiculaeata]
emb|CA002955.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002957.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002959.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002967.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002971.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002972.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002973.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=487

Score = 747 bits (1928), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 363/489 (74%), Positives = 416/489 (85%), Gaps = 4/489 (0%)

Query 54 YIAQSPNFIISNTISNIFDTPSLSTARASNLPEMDKLVKDQVLLVPTVCOCTGNRSFAN 113
Y AQSPPNFIIS+NIS+IP+ SPL IA+ASN+E D KL+ DQ+LLVPTVCOCT N SFAN

Sbjct 1 YIAQSPNFIISNTISNIFDTPSLSTARASNLPEMDKLVKDQVLLVPTVCOCTGNRSFAN 60
YIAQSPNFIISNTISNIFDTPSLSTARASNLPEMDKLVKDQVLLVPTVCOCTGNRSFAN

Query 114 ISYEINGQDSFYVATTSYENLNRWAVMLNFIPLSPKLPIDIGQVVFPLFCCKPSKNQGL 173
+Y I GDS+Y + +TSYANLFW + NP LP LP+ +Y PLFCCKPSKNQGL

Sbjct 61 ITYSIKQDGFILSITSYQNLTYLFENFNPNLSPTLLPDLTKVSVPLFCCKPSKNQGL 120
ITYSIKQDGFILSITSYQNLTYLFENFNPNLSPTLLPDLTKVSVPLFCCKPSKNQGL

Query 174 DKEIKYLITYVMKPGDQNVLSVSKFGASPEDIMSENNYQGNFTAANNLPVLPVTLPLVL 233
+K IKYLITYVM+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIPVT LP L

Sbjct 121 NKGIKYLITYVMQDNNDVTVSSKFGASQVEMLAENH--NFTASTNRSVLIPVTLPLVL 178
NKGIKYLITYVMQDNNDVTVSSKFGASQVEMLAENH--NFTASTNRSVLIPVTLPLVL

Query 234 ARSPSDGRKGIR-LPVIIGISLGCTLLVLVLAVLIVVYCLMKTLNRSASSAETADKL 292
+ 8+GRK + L +IIGISLG +IVL + LVVYCLMK LNRS SS+ETADKL

Sbjct 179 DQSPNSGRKSSQNLALIGISLGSFAFLLVLTLSLVVYCLMKLNRSSTSE 238
DQSPNSGRKSSQNLALIGISLGSFAFLLVLTLSLVVYCLMKLNRSSTSE

Query 293 LAGSGVSGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIGKVLAVKRFKEDVTEELK 352
LAGSGVSGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIGKVLAVKRFKEDVTEELK

Sbjct 239 LAGSGVSGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIGKVLAVKRFKEDVTEELK 298
LAGSGVSGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIGKVLAVKRFKEDVTEELK

Query 353 ILQKVNHNKLMVSSDNDGNCVFVYEAENGSLDEWLFPSKSDTNSRSLTWOOR 412
ILQKVNHNKLMVSSDNDGNCVFVYEAENGSLDEWLFPSKSDTNSRSLTWOOR

Sbjct 299 SEELKILQKVNHNKLMVSSDNDGNCVFVYEAENGSLDEWLFPSKSDTNSRSLTWOOR 357
SEELKILQKVNHNKLMVSSDNDGNCVFVYEAENGSLDEWLFPSKSDTNSRSLTWOOR

Query 413 ISMAVDVAMGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNMMPKID 472
+A+DVA+GLQVMEH YPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNMMPKID

Sbjct 358 ITMAVDVAMGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNMMPKID 417
ITMAVDVAMGLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSGMARTSTNMMPKID

Query 473 VFAPGVLLITGKAMTTKENGVEVVLKMDKFIQDQENREERLRKMMDPKLESYYP 532
VFAPGVLLITGKAMTTKENGVEVVLKMDKFIQDQENREERLRKMMDPKLESYYP

Sbjct 418 VFAPGVLLITGKAMTTKENGVEVVLKMDKFIQDQENREERLRKMMDPKLESYYP 477
VFAPGVLLITGKAMTTKENGVEVVLKMDKFIQDQENREERLRKMMDPKLESYYP

Query 533 IDYALSLAS 541
ID ALS+AS

Sbjct 478 IDNALSMAS 486
IDNALSMAS

>emb|CA002951.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=487

Score = 745 bits (1924), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 363/489 (74%), Positives = 415/489 (84%), Gaps = 4/489 (0%)

Query 54 YIAQSPNFIISNTISNIFDTPSLSTARASNLPEMDKLVKDQVLLVPTVCOCTGNRSFAN 113
Y AQSPPNFIIS+NIS+IP+ SPL IA+ASN+E D KL+ DQ+LLVPTVCOCT N SFAN

Sbjct 1 YIAQSPNFIISNTISNIFDTPSLSTARASNLPEMDKLVKDQVLLVPTVCOCTGNRSFAN 60
YIAQSPNFIISNTISNIFDTPSLSTARASNLPEMDKLVKDQVLLVPTVCOCTGNRSFAN

```

Query 114  ISVEINQGDSPFYVATTSYENLTNWRVAVMDINVLSPNKLPIGIQVVFPLCKPCPSKNQL 173
+Y I GDS+P+ ++ TS+NLN+ ++ NP LSP LP+ +V PLCKPCPSKNQL
Sbjct 61  ITYSIKQDNFTLSTSYQNLTYNLFKPNFNPNSPTLLPLDTKVSVPFLCKPCPSKNQL 120

Query 174  DKELKYLITYVVKPGDVSLSVKFGASPEDIMSENQNTAANNLPVLIPVTLPLVL 233
+K IKYLTIVYV+ DNV+LVS KFGAS +++ENN+ NPTA+ N VLPVTL LP L
Sbjct 121  NKGKYLITYVQNDNVNLTLSVKFGASQVEMLAENN--NFTASTNRSVLIPVTLPL 178

Query 234  ARSPSDRKGGIR-LPVTIGISIGCTLLVLVLAVLIVVYVCLMKMTINRASAETAADKL 292
+S+GRK + L +IGISIG +LVL + LVVYVCLMK LNRS SS+ETADKL
Sbjct 179  DQPSNRGRASSGNLALIGISIGSAFFLIVLTLSLIVVYVCLMKKRIARSTSSETAADKL 238

Query 293  LSGVSGYVKFTMYETDAIMEATMNLSEQCKIGESVYKANIBGVLAVERKFEEDYTEELK 352
+G+G+K + L +IGISIG +LVL + LVVYVCLMK LNRS SS+ETADKL
Sbjct 239  LSGVSGYVKFTMYEIDAMEGTMNLSDNCKIGESVYKANIDGRVLAVERKFEEDYTEELK 296

Query 353  ILQKVNHNGLVKLMGVSSDNDGNCFLVYEAENGSLDEMLFSKSCSDTSSNRASLTWCOR 412
ILQKVNHNGLVKLMGVSSDNDGNCFLVYEAENGSLDEMLFSK+S S TSSN SLTW GR
Sbjct 299  ILQKVNHNGLVKLMGVSSDNDGNCFLVYEAENGSLDEMLFSK+S S TSSN SLTWGR 357

Query 413  ISMAVDVAMGLQYMHREYPRIVHRDITSSNLLDSNFKAKIANFMSMARTFNNMMPKID 472
++A+DVA+GLQYMHREYPRIVHRDITSSNLLDSNFKAKIANF MART TN MPMKID
Sbjct 358  ITAMDAVAILQYMHREYPRIVHRDITSSNLLDSNFKAKIANFMSMARTFNNMMPKID 417

Query 473  VFAFGVLLIELTGRKAMTTKENGSEVVMLMKDIIWKI FDOENREERLKKMDEPKLESYP 532
VFAFGVLLIELTGRKAMTTKENGSEVVMLMKDIIWKI FDOENREERLKKMDEPKLESYP
Sbjct 418  VFAFGVLLIELTGRKAMTTKENGSEVVMLMKDIIWKI FDOENREERLKKMDEPKLESYP 477

Query 533  IDVALSIAS 541
ID ALSIAS
Sbjct 478  IDVALSIAS 486

```

>emb|CA002940.1 LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=487

Score = 745 bits (1923), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 363/489 (74%), Positives = 415/489 (84%), Gaps = 4/489 (0%)

```

Query 54  YIAGSPNPLSLTNISNIFDTPSLTARASNLPMDDKLVDQVLVLPVTCGCTGNRGSFAN 113
Y AGSPNPLSLTNIS+IP+ SPL IA+ASN+E D KL+ DQ+LVLPVTCGCT N SFAN
Sbjct 1  YIAGSPNPLSLTNISNIFDTPSLTARASNLPMDDKLVDQVLVLPVTCGCTGNRGSFAN 60

Query 114  ISVEINQGDSPFYVATTSYENLTNWRVAVMDINVLSPNKLPIGIQVVFPLCKPCPSKNQL 173
+Y I GDS+P+ ++ TS+NLN+ ++ NP LSP LP+ +V PLCKPCPSKNQL
Sbjct 61  ITYSIKQDNFTLSTSYQNLTYNLFKPNFNPNSPTLLPLDTKVSVPFLCKPCPSKNQL 120

Query 174  DKELKYLITYVVKPGDVSLSVKFGASPEDIMSENQNTAANNLPVLIPVTLPLVL 233
+K IKYLTIVYV+ DNV+LVS KFGAS +++ENN+ NPTA+ N VLPVTL LP L
Sbjct 121  NKGKYLITYVQNDNVNLTLSVKFGASQVEMLAENN--NFTASTNRSVLIPVTLPL 178

Query 234  ARSPSDRKGGIR-LPVTIGISIGCTLLVLVLAVLIVVYVCLMKMTINRASAETAADKL 292
+S+GRK + L +IGISIG +LVL + LVVYVCLMK LNRS SS+ETADKL
Sbjct 179  DQPSNRGRASSGNLALIGISIGSAFFLIVLTLSLIVVYVCLMKKRIARSTSSETAADKL 238

Query 293  LSGVSGYVKFTMYETDAIMEATMNLSEQCKIGESVYKANIBGVLAVERKFEEDYTEELK 352
+G+G+K + L +IGISIG +LVL + LVVYVCLMK LNRS SS+ETADKL
Sbjct 239  LSGVSGYVKFTMYEIDAMEGTMNLSDNCKIGESVYKANIDGRVLAVERKFEEDYTEELK 296

Query 353  ILQKVNHNGLVKLMGVSSDNDGNCFLVYEAENGSLDEMLFSKSCSDTSSNRASLTWCOR 412
ILQKVNHNGLVKLMGVSSDNDGNCFLVYEAENGSLDEMLFSK+S S TSSN SLTW GR
Sbjct 299  ILQKVNHNGLVKLMGVSSDNDGNCFLVYEAENGSLDEMLFSK+S S TSSN SLTWGR 357

Query 413  ISMAVDVAMGLQYMHREYPRIVHRDITSSNLLDSNFKAKIANFMSMARTFNNMMPKID 472
++A+DVA+GLQYMHREYPRIVHRDITSSNLLDSNFKAKIANF MART TN MPMKID
Sbjct 358  ITAMDAVAILQYMHREYPRIVHRDITSSNLLDSNFKAKIANFMSMARTFNNMMPKID 417

Query 473  VFAFGVLLIELTGRKAMTTKENGSEVVMLMKDIIWKI FDOENREERLKKMDEPKLESYP 532
VFAFGVLLIELTGRKAMTTKENGSEVVMLMKDIIWKI FDOENREERLKKMDEPKLESYP
Sbjct 418  VFAFGVLLIELTGRKAMTTKENGSEVVMLMKDIIWKI FDOENREERLKKMDEPKLESYP 477

Query 533  IDVALSIAS 541
ID ALSIAS
Sbjct 478  IDVALSIAS 486

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>emb|CA002941.1 LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
>emb|CA002970.1 LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=487

Score = 744 bits (1922), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 362/489 (74%), Positives = 415/489 (84%), Gaps = 4/489 (0%)

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Query 54  YIAGSPNPLSLTNISNIFDTPSLTARASNLPMDDKLVDQVLVLPVTCGCTGNRGSFAN 113
Y AGSPNPLSLTNIS+IP+ SPL IA+ASN+E D KL+ DQ+LVLPVTCGCT N SFAN
Sbjct 1  YIAGSPNPLSLTNISNIFDTPSLTARASNLPMDDKLVDQVLVLPVTCGCTGNRGSFAN 60

Query 114  ISVEINQGDSPFYVATTSYENLTNWRVAVMDINVLSPNKLPIGIQVVFPLCKPCPSKNQL 173
+Y I GDS+P+ ++ TS+NLN+ ++ NP LSP LP+ +V PLCKPCPSKNQL
Sbjct 61  ITYSIKQDNFTLSTSYQNLTYNLFKPNFNPNSPTLLPLDTKVSVPFLCKPCPSKNQL 120

Query 174  DKELKYLITYVVKPGDVSLSVKFGASPEDIMSENQNTAANNLPVLIPVTLPLVL 233
+K IKYLTIVYV+ DNV+LVS KFGAS +++ENN+ NPTA+ N VLPVTL LP L
Sbjct 121  NKGKYLITYVQNDNVNLTLSVKFGASQVEMLAENN--NFTASTNRSVLIPVTLPL 178

Query 234  ARSPSDRKGGIR-LPVTIGISIGCTLLVLVLAVLIVVYVCLMKMTINRASAETAADKL 292
+S+GRK + L +IGISIG +LVL + LVVYVCLMK LNRS SS+ETADKL
Sbjct 179  DQPSNRGRASSGNLALIGISIGSAFFLIVLTLSLIVVYVCLMKKRIARSTSSETAADKL 238

Query 293  LSGVSGYVKFTMYETDAIMEATMNLSEQCKIGESVYKANIBGVLAVERKFEEDYTEELK 352
+G+G+K + L +IGISIG +LVL + LVVYVCLMK LNRS SS+ETADKL
Sbjct 239  LSGVSGYVKFTMYEIDAMEGTMNLSDNCKIGESVYKANIDGRVLAVERKFEEDYTEELK 296

Query 353  ILQKVNHNGLVKLMGVSSDNDGNCFLVYEAENGSLDEMLFSKSCSDTSSNRASLTWCOR 412
ILQKVNHNGLVKLMGVSSDNDGNCFLVYEAENGSLDEMLFSK+S S TSSN SLTWGR

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Sbjct 299 ILQKVNHGNIWKIMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNVSVLTSWSGR 357
ILQKVNHGNIWKIMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNVSVLTSWSGR
Query 413 ISMAVDVAMGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID 472
I+ADVA+GLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID
Sbjct 358 ITIAMDVAGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID 417
ITIAMDVAGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID
Query 473 VFAGVVLIELLTGRKAMTTKENGVEVVMWKIDWKIDQENREERLKKMMPKLESYYP 532
VFAGVVLIELLTGRKAMTTKENGVEVVMWKIDWKIDQENREERLKKMMPKLESYYP
Sbjct 418 VFAGVVLIELLTGRKAMTTKENGVEVVMWKIDWKIDQENREERLKKMMPKLESYYP 477
VFAGVVLIELLTGRKAMTTKENGVEVVMWKIDWKIDQENREERLKKMMPKLESYYP
Query 533 IDVALSLAS 541
ID VALSLAS
Sbjct 478 IDVALSLAS 486
ID VALSLAS

>emb|CAO02966.1| LysM-domain containing receptor-like kinase [Medicago tornata]
Length=467

Score = 741 bits (1914), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 362/489 (74%), Positives = 414/489 (84%), Gaps = 4/489 (0%)

Query 54 YIAGSPNPLISLNTISNIDFTSPSLISARASNLDEWLFSES-SKTSNVSVLTSWSGR 113
YAGSPNPLISLNTISNIDFTSPSLISARASNLDEWLFSES-SKTSNVSVLTSWSGR
Sbjct 1 YIAGSPNPLISLNTISNIDFTSPSLISARASNLDEWLFSES-SKTSNVSVLTSWSGR 60
YIAGSPNPLISLNTISNIDFTSPSLISARASNLDEWLFSES-SKTSNVSVLTSWSGR
Query 114 ISVEINQDSYFVATTSYENLNWRAVMDLNPVLSPNKLPIGQVFPFLCKCPKSNKOL 173
I+Y I CD+P++TSY+NLN+ + NP LSP LP+ +V PLFCCKPSKOL
Sbjct 61 ITYSIKLGNFTILSTISYQNLINYLEFKNPNPILPTLLPLDTPVSVPLFCCKCPKSNKOL 120
ITYSIKLGNFTILSTISYQNLINYLEFKNPNPILPTLLPLDTPVSVPLFCCKCPKSNKOL
Query 174 DKRIYLYTYVMKQDNVLSVDKFGASPEDIMSENNGYQNTAANNLPVLPVTRFLVRL 233
+K IYLYTYVM+ DN+LVS RFKAS +++++NFT+ N VLPVTP LP L
Sbjct 121 NRGSLYLYTYVMKQDNVLSVDKFGASPEDIMSENNGYQNTAANNLPVLPVTRFLVRL 178
NRGSLYLYTYVMKQDNVLSVDKFGASPEDIMSENNGYQNTAANNLPVLPVTRFLVRL
Query 234 ARSPSDRGKQIRL+LPIIGISLGLTLLVLVLAVLIVVYCLAKMTNLRASASATADKL 192
+S+GRK +L+IIGISGL+LVL+LVVYVCLMRK LNRS SS+ETADKL
Sbjct 179 DQPSNGRKSQSLNALLIGISLGSAPFLLVLTLLVYVYCLMRKLNRSSTSSATADKL 238
DQPSNGRKSQSLNALLIGISLGSAPFLLVLTLLVYVYCLMRKLNRSSTSSATADKL
Query 293 LSGVSGVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTEELK 352
LSGVSGVSKPTMYE DAIME TMLNS+ CKIGESVYKANI+GVLAVK+ K+D +EELK
Sbjct 293 LSGVSGVSKPTMYEIDAIMEATMNLSDNCKIGESVYKANIIGKVLAVKRFKEDVTEELK 298
LSGVSGVSKPTMYEIDAIMEATMNLSDNCKIGESVYKANIIGKVLAVKRFKEDVTEELK
Query 353 ILQKVNHGNIWKIMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNVSVLTSWSGR 412
ILQKVNHGNIWKIMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNVSVLTSWSGR
Sbjct 299 ILQKVNHGNIWKIMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNVSVLTSWSGR 357
ILQKVNHGNIWKIMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNVSVLTSWSGR
Query 413 ISMAVDVAMGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID 472
I+ADVA+GLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID
Sbjct 358 ITIAMDVAGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID 417
ITIAMDVAGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID
Query 473 VFAGVVLIELLTGRKAMTTKENGVEVVMWKIDWKIDQENREERLKKMMPKLESYYP 532
VFAGVVLIELLTGRKAMTTKENGVEVVMWKIDWKIDQENREERLKKMMPKLESYYP
Sbjct 418 VFAGVVLIELLTGRKAMTTKENGVEVVMWKIDWKIDQENREERLKKMMPKLESYYP 477
VFAGVVLIELLTGRKAMTTKENGVEVVMWKIDWKIDQENREERLKKMMPKLESYYP
Query 533 IDVALSLAS 541
ID VALSLAS
Sbjct 478 IDVALSLAS 486
ID VALSLAS

>dbj|BAI79275.1| LysM type receptor kinase [Lotus japonicus]

>dbj|BAI79285.1| LysM type receptor kinase [Lotus japonicus]

Length=591

GENE ID: 100380877 Lys11 | LysM type receptor kinase [Lotus japonicus]
(10 or fewer PubMed links)

Score = 704 bits (1817), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 376/606 (62%), Positives = 461/606 (76%), Gaps = 23/606 (3%)

Query 1 MAVFEPFLPLASQILCLVIMLFST---NIVAQSQDNRTNFSKPSDPPSCCTVYTYAQS 58
M EF P + + +M FST +I+AQ N TNFSCP DSSPSC+TVTY AQS
Sbjct 1 MFSFELFT---NTLFLANMFSTTHHILAQLSHTNGTNFSKPSDPPSCCTVYTYAQS 57
MFSFELFT---NTLFLANMFSTTHHILAQLSHTNGTNFSKPSDPPSCCTVYTYAQS
Query 59 NPLSLNTISNIDFTSPSLISARASNLDEWLFSES-SKTSNVSVLTSWSGR 118
NPLSLNTISNIDFTSPSLISARASNLDEWLFSES-SKTSNVSVLTSWSGR
Sbjct 58 NPLSLNTISNIDFTSPSLISARASNLDEWLFSES-SKTSNVSVLTSWSGR 117
NPLSLNTISNIDFTSPSLISARASNLDEWLFSES-SKTSNVSVLTSWSGR
Query 119 NQGDSEYFVATTSYENLNWRAVMDLNPVLSPNKLPIGQVFPFLCKCPKSNKOLDEIK 178
+G+S+Y++TSYENLNW V D NP +P LP+G+VW PLFCCKPS L+K+I
Sbjct 118 KEGESYIYLTSTSYENLNWETVQDSNPYNYFLLPVGIKVLPFLCKCPKSNYHLNKGIE 177
KEGESYIYLTSTSYENLNWETVQDSNPYNYFLLPVGIKVLPFLCKCPKSNYHLNKGIE
Query 179 YLYTYVMKQDNVLSVDKFGASPEDIMSENNGYQNTAANNLPVLPVTRFLVRL 237
YLYTYVM DNVSIV+ KFG S +DI+SENN+ QNTAA N P+LPIVTP LP L+G
Sbjct 178 YLYTYVMKQDNVLSVDKFGASPEDIMSENNGYQNTAANNLPVLPVTRFLVRL 237
YLYTYVMKQDNVLSVDKFGASPEDIMSENNGYQNTAANNLPVLPVTRFLVRL
Query 238 SDGRKSGIRLPLVIGISLGLTLLVLVLAVL+LVVYVCLMRK---TLNRASASASTA-DKLL 293
+S+R+L LV V CL+ + N+S +S +S K+L
Sbjct 238 SSSERKSNRHHIIIGISLGSLLTLLALLVLSVTPCLRRKRSSENKLLSVEIAGLKL 297
SSSERKSNRHHIIIGISLGSLLTLLALLVLSVTPCLRRKRSSENKLLSVEIAGLKL
Query 294 SGVSGVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTEELK 353
SGVS YVSK +YE IMEAT+NL+EQCKIGESVYK +G+VLAVK+ KEDVTEE+ I
Sbjct 294 SGVSGVSKPTMYEIDFRLMEATMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTEELK 357
SGVSGVSKPTMYEIDFRLMEATMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTEELK
Query 354 LQKVNHGNIWKIMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNVSVLTSWSGR 413
LQKVNHGNIWKIMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNVSVLTSWSGR
Sbjct 358 LQKVNHGNIWKIMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNVSVLTSWSGR 417
LQKVNHGNIWKIMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNVSVLTSWSGR
Query 413 ISMAVDVAMGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID 472
I+ADVA+GLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID
Sbjct 358 ITIAMDVAGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID 417
ITIAMDVAGLQYMHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFNNMMPKID
Query 473 VFAGVVLIELLTGRKAMTTKENGVEVVMWKIDWKIDQENREERLKKMMPKLESYYP 532
P+GVVL+ELL+G+K+T N E+ I +FD +E REER++WMDER+ES YPI
Sbjct 474 FQYGVVLIELLGSKKSLT---NNEI---NHIREIFDLKEREERLKKMMPKLESYYP 536
FQYGVVLIELLGSKKSLT---NNEI---NHIREIFDLKEREERLKKMMPKLESYYP
Query 534 IDVALSLASLAVNCTADKSLRPT+AEVLISLIL+TQPSBATLERSLSSGLDVEATQIV 592
D ALSLA L+AVNCT+K LSRPT+ E+VLISLIL TQ SP TERS Y GLDV+ Y++
D ALSLA L+AVNCT+K LSRPT+ E+VLISLIL TQ SP TERS Y GLDV+ Y++

Sbjct 527 DDALSLAFLAMNCTSEKPLSRPTMGHVVLISLLMTQHSPTTLERSGWT-CGLDWDVTEMQ 585
 Query 593 TSIAAR 598
 T IAAR
 Sbjct 586 TLIAAR 591

>gb|ADJ19109.1| **G** truncated Nod-factor receptor 5A [Glycine max]
 Length=337
 GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
 (10 or fewer PubMed links)
 Score = 695 bits (1793), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 337/337 (100%), Positives = 337/337 (100%), Gaps = 0/337 (0%)

Query 1 MAVFPPFLPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFCSPSDSPFCSETTYVTYIAQSFN 60
 Sbjct 1 MAVFPPFLPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFCSPSDSPFCSETTYVTYIAQSFN 60
 MAVFPPFLPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFCSPSDSPFCSETTYVTYIAQSFN 60
 Query 61 FLSLNTISNIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQ 120
 FLSLNTISNIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQ 120
 FLSLNTISNIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQ 120
 Sbjct 61 FLSLNTISNIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQ 120
 Query 121 GDSFYFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYL 180
 GDSFYFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYL 180
 GDSFYFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYL 180
 Sbjct 121 GDSFYFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYL 180
 Query 181 ITYVWRPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDG 240
 ITYVWRPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDG 240
 ITYVWRPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDG 240
 Sbjct 181 ITYVWRPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDG 240
 Query 241 RKQIRLPVIGISLQCTLLVLVAVLLVYVYCLRMKTNIRASSAETAADKLLSGVSGYV 300
 RKQIRLPVIGISLQCTLLVLVAVLLVYVYCLRMKTNIRASSAETAADKLLSGVSGYV 300
 RKQIRLPVIGISLQCTLLVLVAVLLVYVYCLRMKTNIRASSAETAADKLLSGVSGYV 300
 Sbjct 241 RKQIRLPVIGISLQCTLLVLVAVLLVYVYCLRMKTNIRASSAETAADKLLSGVSGYV 300
 Query 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKV 337
 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKV 337
 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKV 337
 Sbjct 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKV 337

>dbj|BAG85143.1| Nod factor receptor protein [Glycine soja]
 >dbj|BAG85149.1| Nod factor receptor protein [Glycine soja]
 >dbj|BAG85156.1| Nod factor receptor protein [Glycine soja]
 11 more sequence titles

>dbj|BAG85159.1| Nod factor receptor protein [Glycine max]
 >dbj|BAG85160.1| Nod factor receptor protein [Glycine max]
 >dbj|BAG85161.1| Nod factor receptor protein [Glycine max]
 >dbj|BAG85162.1| Nod factor receptor protein [Glycine max]
 >dbj|BAG85165.1| Nod factor receptor protein [Glycine max]
 >dbj|BAG85169.1| Nod factor receptor protein [Glycine max]
 >dbj|BAG85171.1| Nod factor receptor protein [Glycine max]
 >dbj|BAG85174.1| Nod factor receptor protein [Glycine max]
 >dbj|BAG85177.1| **G** Nod factor receptor protein [Glycine max]
 >dbj|BAG85179.1| Nod factor receptor protein [Glycine max]
 >dbj|BAG85180.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 675 bits (1741), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 327/327 (100%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5 FPFPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFCSPSDSPFCSETTYVTYIAQSFN 64
 Sbjct 1 FPFPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFCSPSDSPFCSETTYVTYIAQSFN 64
 FPFPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFCSPSDSPFCSETTYVTYIAQSFN 64
 Query 65 TNSINIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQDGF 124
 TNSINIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQDGF 124
 TNSINIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQDGF 120
 Sbjct 61 TNSINIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQDGF 120
 Query 125 YFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYLITV 184
 YFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYLITV 184
 YFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYLITV 180
 Sbjct 125 YFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYLITV 180
 Query 185 WKPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDGRGG 244
 WKPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDGRGG 244
 WKPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDGRGG 240
 Sbjct 181 WKPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDGRGG 240
 Query 245 IRLPVIIGISLQCTLLVLVAVLLVYVYCLRMKTNIRASSAETAADKLLSGVSGVSKPT 304
 IRLPVIIGISLQCTLLVLVAVLLVYVYCLRMKTNIRASSAETAADKLLSGVSGVSKPT 304
 IRLPVIIGISLQCTLLVLVAVLLVYVYCLRMKTNIRASSAETAADKLLSGVSGVSKPT 300
 Sbjct 241 IRLPVIIGISLQCTLLVLVAVLLVYVYCLRMKTNIRASSAETAADKLLSGVSGVSKPT 300
 Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 MYETDAIMEATMNLSEQCKIGESVYKA 331
 MYETDAIMEATMNLSEQCKIGESVYKA 327
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85148.1| Nod factor receptor protein [Glycine soja]
 Length=327
 Score = 674 bits (1739), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5 FPFPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFCSPSDSPFCSETTYVTYIAQSFN 64
 Sbjct 1 FPFPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFCSPSDSPFCSETTYVTYIAQSFN 64
 FPFPLHSQILCLVIMLFSTNIVAQSQDQNRNTNFCSPSDSPFCSETTYVTYIAQSFN 60
 Query 65 TNSINIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQDGF 124
 TNSINIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQDGF 124
 TNSINIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQDGF 120
 Sbjct 61 TNSINIFDTSPLSIARASNLPMDDKLVKDQVLLVFPVTCGCTGNRSFANISYEINQDGF 120
 Query 125 YFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYLITV 184
 YFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYLITV 184
 YFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYLITV 180
 Sbjct 121 YFVATTSYENLTNRWAVMDLNPVLSPNKLPIGIQVFFFLCKCPSKNQLDKEIKYLITV 180
 Query 185 WKPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDGRGG 244
 WKPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDGRGG 244
 WKPGDNVLSVDKFGASPEDIMSENNYQGNFTANNLPVLPVTRLPVLARSFSDGRGG 244

Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLFVLARSFSDGRKG 240
 Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
 Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 MYETDAIMEATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085151.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5 FPFLLPLHSQICLIVIMLFSTNIVAQSQDNRNTFSCPSDSPSCETVYVYIAQSPNFLSL 64
 FPFLLPLHSQICLIVIMLFSTNIVAQSQDNRNTFSCPSDSPSCETVYVYIAQSPNFLSL
 Sbjct 1 FPFLLPLHSQICLIVIMLFSTNIVAQSQDNRNTFSCPSDSPSCETVYVYIAQSPNFLSL 60
 Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLVPVTCGCTGNRSFANIYSVEINQGDSE 124
 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLVPVTCGCTGNRSFANIYSVEINQGDSE
 Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLVPVTCGCTGNRSFANIYSVEINQGDSE 120
 Query 125 YFVATTSYENITNWRAMVDLNPVLSNKLPIGIGVVFPLFCCKPSKNQLDREIKYLITV 184
 YFVATTSYENITNWRAMVDLNPVLSNKLPIGIGVVFPLFCCKPSKNQLDREIKYLITV
 Sbjct 121 YFVATTSYENITNWRAMVDLNPVLSNKLPIGIGVVFPLFCCKPSKNQLDREIKYLITV 180
 Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLFVLARSFSDGRKG 244
 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLFVLARSFSDGRKG
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLFVLARSFSDGRKG 240
 Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
 Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 MYETDAIMEATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085178.1| Nod factor receptor protein [Glycine max]
 Length=327

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
 (10 or fewer PubMed links)

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5 FPFLLPLHSQICLIVIMLFSTNIVAQSQDNRNTFSCPSDSPSCETVYVYIAQSPNFLSL 64
 FPFLLPLHSQICLIVIMLFSTNIVAQSQDNRNTFSCPSDSPSCETVYVYIAQSPNFLSL
 Sbjct 1 FPFLLPLHSQICLIVIMLFSTNIVAQSQDNRNTFSCPSDSPSCETVYVYIAQSPNFLSL 60
 Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLVPVTCGCTGNRSFANIYSVEINQGDSE 124
 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLVPVTCGCTGNRSFANIYSVEINQGDSE
 Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLVPVTCGCTGNRSFANIYSVEINQGDSE 120
 Query 125 YFVATTSYENITNWRAMVDLNPVLSNKLPIGIGVVFPLFCCKPSKNQLDREIKYLITV 184
 YFVATTSYENITNWRAMVDLNPVLSNKLPIGIGVVFPLFCCKPSKNQLDREIKYLITV
 Sbjct 121 YFVATTSYENITNWRAMVDLNPVLSNKLPIGIGVVFPLFCCKPSKNQLDREIKYLITV 180
 Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLFVLARSFSDGRKG 244
 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLFVLARSFSDGRKG
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLFVLARSFSDGRKG 240
 Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
 Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 MYETDAIMEATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085167.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFLLPLHSQICLIVIMLFSTNIVAQSQDNRNTFSCPSDSPSCETVYVYIAQSPNFLSL 64
 FPFLLPLHSQICLIVIMLFSTNIVAQSQDNRNTFSCPSDSPSCETVYVYIAQSPNFLSL
 Sbjct 1 FPFLLPLHSQICLIVIMLFSTNIVAQSQDNRNTFSCPSDSPSCETVYVYIAQSPNFLSL 60
 Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLVPVTCGCTGNRSFANIYSVEINQGDSE 124
 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLVPVTCGCTGNRSFANIYSVEINQGDSE
 Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKQVLLVPVTCGCTGNRSFANIYSVEINQGDSE 120
 Query 125 YFVATTSYENITNWRAMVDLNPVLSNKLPIGIGVVFPLFCCKPSKNQLDREIKYLITV 184
 YFVATTSYENITNWRAMVDLNPVLSNKLPIGIGVVFPLFCCKPSKNQLDREIKYLITV
 Sbjct 121 YFVATTSYENITNWRAMVDLNPVLSNKLPIGIGVVFPLFCCKPSKNQLDREIKYLITV 180
 Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLFVLARSFSDGRKG 244
 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLFVLARSFSDGRKG
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLFVLARSFSDGRKG 240
 Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
 Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 MYETDAIMEATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085164.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL 64
FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL 60

Query 65 TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 124
TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF
Sbjct 61 TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120

Query 125 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVQVFFLCCKPSKNQLDKEIKYLITV 184
YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVQVFFLCCKPSKNQLDKEIKYLITV
Sbjct 121 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVQVFFLCCKPSKNQLDKEIKYLITV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATANNLPVLPVTRLPVLARSPDGRGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYQNFATANNLPVLPVTRLPVLARSPDGRGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATANNLPVLPVTRLPVLARSPDGRGG 240

Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKI GESVYKA 331
MYE DAIMEATMNLSEQCKI GESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKI GESVYKA 327

>dbj|BA085170.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 672 bits (1735), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL 64
FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL 60

Query 65 TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 124
TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF
Sbjct 61 TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120

Query 125 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVQVFFLCCKPSKNQLDKEIKYLITV 184
YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVQVFFLCCKPSKNQLDKEIKYLITV
Sbjct 121 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVQVFFLCCKPSKNQLDKEIKYLITV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATANNLPVLPVTRLPVLARSPDGRGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYQNFATANNLPVLPVTRLPVLARSPDGRGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATANNLPVLPVTRLPVLARSPDGRGG 240

Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKI GESVYKA 331
MYETDAIMEATMNLSEQCKI GESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKI GESVYKA 327

>dbj|BA085146.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 672 bits (1735), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL 64
FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL 60

Query 65 TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 124
TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF
Sbjct 61 TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120

Query 125 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVQVFFLCCKPSKNQLDKEIKYLITV 184
YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVQVFFLCCKPSKNQLDKEIKYLITV
Sbjct 121 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVQVFFLCCKPSKNQLDKEIKYLITV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATANNLPVLPVTRLPVLARSPDGRGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYQNFATANNLPVLPVTRLPVLARSPDGRGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATANNLPVLPVTRLPVLARSPDGRGG 240

Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKI GESVYKA 331
MYETDAIMEATMNLSEQCKI GESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKI GESVYKA 327

>dbj|BA085158.1| Nod factor receptor protein [Glycine max]
Length=327

GENE ID: 100301877 nfr5a | Nod factor receptor protein [Glycine max]
(10 or fewer PubMed links)

Score = 672 bits (1735), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL 64
FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQILCLVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCSETTYVTYIAQSPNFLSL 60

Query 65 TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 124
TNISNIDFSPSLIARASNLPEMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF


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Sbjct 61 TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF 120
TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF
Query 125 YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV 184
YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV
Sbjct 121 YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV 180
YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV
Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG 240
WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG
Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
MYETDAIMEATMNLSEQCKIGESVYKA

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>dbj|BA085144.1| Nod factor receptor protein [Glycine soja]
>dbj|BA085145.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 672 bits (1734), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL 64
FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL 60
FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL
Query 65 TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF 124
TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF
Sbjct 61 TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF 120
TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF
Query 125 YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV 184
YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV
Sbjct 121 YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV 180
YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV
Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG 240
WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG
Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
MYETDAIMEATMNLSEQCKIGESVYKA

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>dbj|BA085142.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 672 bits (1734), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL 64
FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL 60
FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL
Query 65 TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF 124
TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF
Sbjct 61 TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF 120
TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF
Query 125 YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV 184
YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV
Sbjct 121 YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV 180
YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV
Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG 240
WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG
Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
MYETDAIMEATMNLSEQCKIGESVYKA

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>dbj|BA085152.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 672 bits (1733), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL 64
FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL 60
FPFPLPLHSQICLIVLMFSTNIVAQSQDNRNTFSCPSDSPSCSETTYVTYIAQSPNFLSL
Query 65 TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF 124
TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF
Sbjct 61 TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF 120
TNSINIFDTSPLSIARASNLPEMDDKLVKDQVLLVPTVCGCTGNRSFANISYEINQGDGF
Query 125 YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV 184
YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV
Sbjct 121 YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV 180
YFVATTSYENITNWRAMVDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITVV
Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG 240
WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPVLPVTRLPVLARSFSDGRKGG
Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT

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Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085175.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 672 bits (1733), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 325/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCETTYVTYIAQSPNFLSL 64
 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRT F+CPDSPPSCETTYVTYIAQSPNFLSL
 Sbjct 1 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTFCTCPDSPPSCETTYVTYIAQSPNFLSL 60

Query 65 TNISNI FDTSPSLIARASNLPEMDCKLVKDQVLLVPVTCGCTGNRSFANISYEINQGSDF 124
 TNISNI FDTSPSLIARASNLPEMDCKLVKDQVLLVPVTCGCTGNRSFANISYEINQGSDF
 Sbjct 61 TNISNI FDTSPSLIARASNLPEMDCKLVKDQVLLVPVTCGCTGNRSFANISYEINQGSDF 120

Query 125 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVVFPFLCKCPKSNQLDKIKYLITTV 184
 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVVFPFLCKCPKSNQLDKIKYLITTV
 Sbjct 121 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVVFPFLCKCPKSNQLDKIKYLITTV 180

Query 185 WKPDGNVSLVSDKFGASPEDIMSENNYQNFTAAANLPVLPVTRLPVLARSPPDGRGG 244
 WKPDGNVSLVSDKFGASPEDIMSENNYQNFTAAANLPVLPVTRLPVLARSPPDGRGG
 Sbjct 181 WKPDGNVSLVSDKFGASPEDIMSENNYQNFTAAANLPVLPVTRLPVLARSPPDGRGG 240

Query 245 IRLPVIIGISIGCTLLVILAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
 IRLPVIIGISIGCTLLVILAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVILAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085172.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 671 bits (1732), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCETTYVTYIAQSPNFLSL 64
 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCETTYVTYIAQSPNFLSL
 Sbjct 1 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCETTYVTYIAQSPNFLSL 60

Query 65 TNISNI FDTSPSLIARASNLPEMDCKLVKDQVLLVPVTCGCTGNRSFANISYEINQGSDF 124
 TNISNI FDTSPSLIARASNLPEMDCKLVKDQVLLVPVTCGCTGNRSFANISYEINQGSDF
 Sbjct 61 TNISNI FDTSPSLIARASNLPEMDCKLVKDQVLLVPVTCGCTGNRSFANISYEINQGSDF 120

Query 125 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVVFPFLCKCPKSNQLDKIKYLITTV 184
 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVVFPFLCKCPKSNQLDKIKYLITTV
 Sbjct 121 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVVFPFLCKCPKSNQLDKIKYLITTV 180

Query 185 WKPDGNVSLVSDKFGASPEDIMSENNYQNFTAAANLPVLPVTRLPVLARSPPDGRGG 244
 WKPDGNVSLVSDKFGASPEDIMSENNYQNFTAAANLPVLPVTRLPVLARSPPDGRGG
 Sbjct 181 WKPDGNVSLVSDKFGASPEDIMSENNYQNFTAAANLPVLPVTRLPVLARSPPDGRGG 240

Query 245 IRLPVIIGISIGCTLLVILAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
 IRLPVIIGISIGCTLLVILAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVILAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085157.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 671 bits (1731), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCETTYVTYIAQSPNFLSL 64
 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCETTYVTYIAQSPNFLSL
 Sbjct 1 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCETTYVTYIAQSPNFLSL 60

Query 65 TNISNI FDTSPSLIARASNLPEMDCKLVKDQVLLVPVTCGCTGNRSFANISYEINQGSDF 124
 TNISNI FDTSPSLIARASNLPEMDCKLVKDQVLLVPVTCGCTGNRSFANISYEINQGSDF
 Sbjct 61 TNISNI FDTSPSLIARASNLPEMDCKLVKDQVLLVPVTCGCTGNRSFANISYEINQGSDF 120

Query 125 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVVFPFLCKCPKSNQLDKIKYLITTV 184
 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVVFPFLCKCPKSNQLDKIKYLITTV
 Sbjct 121 YFVATTSYENITNWRAMVDNLPVLSNKLPIGIVVFPFLCKCPKSNQLDKIKYLITTV 180

Query 185 WKPDGNVSLVSDKFGASPEDIMSENNYQNFTAAANLPVLPVTRLPVLARSPPDGRGG 244
 WKPDGNVSLVSDKFGASPEDIMSENNYQNFTAAANLPVLPVTRLPVLARSPPDGRGG
 Sbjct 181 WKPDGNVSLVSDKFGASPEDIMSENNYQNFTAAANLPVLPVTRLPVLARSPPDGRGG 240

Query 245 IRLPVIIGISIGCTLLVILAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
 IRLPVIIGISIGCTLLVILAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVILAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085150.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 671 bits (1731), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCETTYVTYIAQSPNFLSL 64
 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCETTYVTYIAQSPNFLSL
 Sbjct 1 FPFPLPLHSQICLIVIMLFSTNI VAQSQQDNRTNFSCPSDSPSCETTYVTYIAQSPNFLSL 60

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Query 65  TNSISIFDTSPLSIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 124
Sbjct 61  TNSISIFDTSPLSIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 120
Query 125  YFVATTSYENITNWRAMVDINPVLSPNKLPIGIGVVFPLFCKCPSKNQLDKEIKYLITTV 184
Sbjct 121  YFVATTSYENITNWRAMVDINPVLSPNKLPIGIGVVFPLFCKCPSKNQLDKEIKYLITTV 180
Query 185  WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPLVLPVTRLFVLARSPDGRGKG 244
Sbjct 181  WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPLVLPVTRLFVLARSPDGRGKG 240
Query 245  IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
Sbjct 241  IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
Query 305  MYETAIMEATMNLSEQCKIGESVYKA 331
Sbjct 301  MYETAIMEATMNLSEQCKIGESVYKA 327

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>dbj|BA085176.1| Nod factor receptor protein [Glycine max]
Length=327
Score = 670 bits (1728), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)
Query 5  FPFPLPLHSQILCLVIMLFSTNIVAQSQDQNRNFCSPDSPPSCETTYVTYIAQSPNFLSL 64
Sbjct 1  FPFPLPLHSQILCLVIMLFSTNIVAQSQDQNRNFCSPDSPPSCETTYVTYIAQSPNFLSL 60
Query 65  TNSISIFDTSPLSIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 124
Sbjct 61  TNSISIFDTSPLSIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 120
Query 125  YFVATTSYENITNWRAMVDINPVLSPNKLPIGIGVVFPLFCKCPSKNQLDKEIKYLITTV 184
Sbjct 121  YFVATTSYENITNWRAMVDINPVLSPNKLPIGIGVVFPLFCKCPSKNQLDKEIKYLITTV 180
Query 185  WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPLVLPVTRLFVLARSPDGRGKG 244
Sbjct 181  WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPLVLPVTRLFVLARSPDGRGKG 240
Query 245  IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
Sbjct 241  IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
Query 305  MYETAIMEATMNLSEQCKIGESVYKA 331
Sbjct 301  MYETAIMEATMNLSEQCKIGESVYKA 327

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>dbj|BA085155.1| Nod factor receptor protein [Glycine soja]
Length=327
Score = 669 bits (1727), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)
Query 5  FPFPLPLHSQILCLVIMLFSTNIVAQSQDQNRNFCSPDSPPSCETTYVTYIAQSPNFLSL 64
Sbjct 1  FPFPLPLHSQILCLVIMLFSTNIVAQSQDQNRNFCSPDSPPSCETTYVTYIAQSPNFLSL 60
Query 65  TNSISIFDTSPLSIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 124
Sbjct 61  TNSISIFDTSPLSIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 120
Query 125  YFVATTSYENITNWRAMVDINPVLSPNKLPIGIGVVFPLFCKCPSKNQLDKEIKYLITTV 184
Sbjct 121  YFVATTSYENITNWRAMVDINPVLSPNKLPIGIGVVFPLFCKCPSKNQLDKEIKYLITTV 180
Query 185  WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPLVLPVTRLFVLARSPDGRGKG 244
Sbjct 181  WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPLVLPVTRLFVLARSPDGRGKG 240
Query 245  IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
Sbjct 241  IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
Query 305  MYETAIMEATMNLSEQCKIGESVYKA 331
Sbjct 301  MYETAIMEATMNLSEQCKIGESVYKA 327

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>dbj|BA085155.1| Nod factor receptor protein [Glycine soja]
Length=327
Score = 669 bits (1726), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)
Query 5  FPFPLPLHSQILCLVIMLFSTNIVAQSQDQNRNFCSPDSPPSCETTYVTYIAQSPNFLSL 64
Sbjct 1  FPFPLPLHSQILCLVIMLFSTNIVAQSQDQNRNFCSPDSPPSCETTYVTYIAQSPNFLSL 60
Query 65  TNSISIFDTSPLSIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 124
Sbjct 61  TNSISIFDTSPLSIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 120
Query 125  YFVATTSYENITNWRAMVDINPVLSPNKLPIGIGVVFPLFCKCPSKNQLDKEIKYLITTV 184
Sbjct 121  YFVATTSYENITNWRAMVDINPVLSPNKLPIGIGVVFPLFCKCPSKNQLDKEIKYLITTV 180
Query 185  WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPLVLPVTRLFVLARSPDGRGKG 244
Sbjct 181  WKPGDNVSLVSDKFGASPEDIMSENNYQGNPTAANNLPLVLPVTRLFVLARSPDGRGKG 240
Query 245  IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
Sbjct 241  IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300

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Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
 Query 305 MYETDAIMEATNNLSEQCKIGESVYKA 331
 MYTDAIMEATNNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATNNLSEQCKIGESVYKA 327

>dbj|BA08163.1| Nod factor receptor protein [Glycine max]
 Length=327
 Score = 669 bits (1726), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL 64
 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL
 Sbjct 1 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL 60
 Query 65 TNISNIFDTSPLSARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 124
 TNISNIFDTSPLSARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF
 Sbjct 61 TNISNIFDTSPLSARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120
 Query 125 YFVATTSYENITNWRAMVDNLNPLSPNKLPIGIQVFPFLCKCPSKNQLDKEIKYLITTV 184
 YFVATTSYENITNWRAMVDNLNPLSPNKLPIGIQVFPFLCKCPSKNQLDKEIKYLITTV
 Sbjct 121 YFVATTSYENITNWRAMVDNLNPLSPNKLPIGIQVFPFLCKCPSKNQLDKEIKYLITTV 180
 Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNTAANNLPLVLPVTRLVPLARSPSDGRGG 244
 WKPGDNVSLVSDKFGASPEDIMSENNYQNTAANNLPLVLPVTRLVPLARSPSDGRGG
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNTAANNLPLVLPVTRLVPLARSPSDGRGG 240
 Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
 Query 305 MYETDAIMEATNNLSEQCKIGESVYKA 331
 MYTDAIMEATNNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATNNLSEQCKIGESVYKA 327

>dbj|BA08151.1| Nod factor receptor protein [Glycine max]
 Length=327
 Score = 669 bits (1725), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL 64
 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL
 Sbjct 1 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL 60
 Query 65 TNISNIFDTSPLSARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 124
 TNISNIFDTSPLSARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF
 Sbjct 61 TNISNIFDTSPLSARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120
 Query 125 YFVATTSYENITNWRAMVDNLNPLSPNKLPIGIQVFPFLCKCPSKNQLDKEIKYLITTV 184
 YFVATTSYENITNWRAMVDNLNPLSPNKLPIGIQVFPFLCKCPSKNQLDKEIKYLITTV
 Sbjct 121 YFVATTSYENITNWRAMVDNLNPLSPNKLPIGIQVFPFLCKCPSKNQLDKEIKYLITTV 180
 Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNTAANNLPLVLPVTRLVPLARSPSDGRGG 244
 WKPGDNVSLVSDKFGASPEDIMSENNYQNTAANNLPLVLPVTRLVPLARSPSDGRGG
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNTAANNLPLVLPVTRLVPLARSPSDGRGG 240
 Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
 Query 305 MYETDAIMEATNNLSEQCKIGESVYKA 331
 MYTDAIMEATNNLSEQCKIGESVYKA
 Sbjct 301 MYTDAIMEATNNLSEQCKIGESVYKA 327

>dbj|BA08154.1| Nod factor receptor protein [Glycine soja]
 Length=327
 Score = 667 bits (1720), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 324/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL 64
 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL
 Sbjct 1 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL 60
 Query 65 TNISNIFDTSPLSARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 124
 TNISNIFDTSPLSARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF
 Sbjct 61 TNISNIFDTSPLSARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120
 Query 125 YFVATTSYENITNWRAMVDNLNPLSPNKLPIGIQVFPFLCKCPSKNQLDKEIKYLITTV 184
 YFVATTSYENITNWRAMVDNLNPLSPNKLPIGIQVFPFLCKCPSKNQLDKEIKYLITTV
 Sbjct 121 YFVATTSYENITNWRAMVDNLNPLSPNKLPIGIQVFPFLCKCPSKNQLDKEIKYLITTV 180
 Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNTAANNLPLVLPVTRLVPLARSPSDGRGG 244
 WKPGDNVSLVSDKFGASPEDIMSENNYQNTAANNLPLVLPVTRLVPLARSPSDGRGG
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNTAANNLPLVLPVTRLVPLARSPSDGRGG 240
 Query 245 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT
 Sbjct 241 IRLPVIIGISIGCTLLVLVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
 Query 305 MYETDAIMEATNNLSEQCKIGESVYKA 331
 MYTDAIMEATNNLSEQCKIGESVYKA
 Sbjct 301 MYTDAIMEATNNLSEQCKIGESVYKA 327

>dbj|BA08169.1| Nod factor receptor protein [Glycine max]
 Length=327
 Score = 665 bits (1717), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 324/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL 64
 FPFPLPLHSQIICLVIMLFSTNIVAQSQDQNRNTFSCPSDSPSCETTYVTYIAQSPNFLSL

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Sbjct 1   FFPLPLHSQICLIVIMLFSTNIVAQSQQNRNTNFCSPDSPFSCETYVTYIAQSPNFLSL 60
Query 65   TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 124
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120
Sbjct 61   TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120
Query 125   YFVATTSYENITNRRAMVDINPVLSPNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITV 184
          YFVATTSYENITNRRAMVDINPVLSPNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITV 180
Sbjct 121   YFVATTSYENITNRRAMVDINPVLSPNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITV 180
Query 185   WKPGDNVSLVBDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLPVLARSPDGRGKG 244
          WKPGDNVSLVBDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLPVLARSPDGRGKG 240
Sbjct 181   WKPGDNVSLVBDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLPVLARSPDGRGKG 240
Query 245   IRLPVIIGISGCTLLVLIVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
          IRLPVIIGISGCTLLVLIVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
Sbjct 241   IRLPVIIGISGCTLLVLIVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
Query 305   MYETDAIMEATMNLSECKIGESVYKA 331
          MYETDAIMEATMNLSECKIGESVYKA
Sbjct 301   MYETDAIMEATMNLSECKIGESVYKA 327

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>dbj|BA085166.1| Nod factor receptor protein [Glycine max]
length=327

Score = 660 bits (1702), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 320/324 (98%), Positives = 322/324 (99%), Gaps = 0/324 (0%)

Query 5   FFPLPLHSQICLIVIMLFSTNIVAQSQQNRNTNFCSPDSPFSCETYVTYIAQSPNFLSL 64
          FFPLPLHSQICLIVIMLFSTNIVAQSQQNRNTNFCSPDSPFSCETYVTYIAQSPNFLSL
Sbjct 1   FFPLPLHSQICLIVIMLFSTNIVAQSQQNRNTNFCSPDSPFSCETYVTYIAQSPNFLSL 60
Query 65   TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 124
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120
Sbjct 61   TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120
Query 125   YFVATTSYENITNRRAMVDINPVLSPNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITV 184
          YFVATTSYENITNRRAMVDINPVLSPNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITV 180
Sbjct 121   YFVATTSYENITNRRAMVDINPVLSPNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITV 180
Query 185   WKPGDNVSLVBDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLPVLARSPDGRGKG 244
          WKPGDNVSLVBDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLPVLARSPDGRGKG 240
Sbjct 181   WKPGDNVSLVBDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLPVLARSPDGRGKG 240
Query 245   IRLPVIIGISGCTLLVLIVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
          IRLPVIIGISGCTLLVLIVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
Sbjct 241   IRLPVIIGISGCTLLVLIVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
Query 305   MYETDAIMEATMNLSECKIGESV 328
          MYETDAIMEATMNLSECKIGESV
Sbjct 301   MYETDAIMEATMNLSECKIGESV 324

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>dbj|BA085147.1| Nod factor receptor protein [Glycine soja]
length=327

Score = 659 bits (1703), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 320/327 (97%), Positives = 321/327 (98%), Gaps = 0/327 (0%)

Query 5   FFPLPLHSQICLIVIMLFSTNIVAQSQQNRNTNFCSPDSPFSCETYVTYIAQSPNFLSL 64
          FFPLPLHSQICLIVIMLFSTNIVAQSQQNRNTNFCSPDSPFSCETYVTYIAQSPNFLSL
Sbjct 1   FFPLPLHSQICLIVIMLFSTNIVAQSQQNRNTNFCSPDSPFSCETYVTYIAQSPNFLSL 60
Query 65   TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 124
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120
Sbjct 61   TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDGF 120
Query 125   YFVATTSYENITNRRAMVDINPVLSPNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITV 184
          YFVATTSYENITNRRAMVDINPVLSPNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITV 180
Sbjct 121   YFVATTSYENITNRRAMVDINPVLSPNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITV 180
Query 185   WKPGDNVSLVBDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLPVLARSPDGRGKG 244
          WKPGDNVSLVBDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLPVLARSPDGRGKG 240
Sbjct 181   WKPGDNVSLVBDKFGASPEDIMSENNYQGNPTAANNLPVLIPVTRLPVLARSPDGRGKG 240
Query 245   IRLPVIIGISGCTLLVLIVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 304
          IRLPVIIGISGCTLLVLIVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
Sbjct 241   IRLPVIIGISGCTLLVLIVLAVLLVYVYCLMKMTINRSASSAETADKLLSGVSGVSKPT 300
Query 305   MYETDAIMEATMNLSECKIGESVYKA 331
          MYETDAIMEATMNLSECKIGESVYKA
Sbjct 301   MYETDAIMEATMNLSECKIGESVYKA 327

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>ref|XP_002269472.1| [NC] PREDICTED: hypothetical protein [Vitis vinifera]
emb|CB117584.3| [E] unnamed protein product [Vitis vinifera]
length=500

GENE ID: 100259809 LOC100259809 | hypothetical protein LOC100259809
[Vitis vinifera] (10 or fewer PubMed links)

Score = 654 bits (1688), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 341/579 (58%), Positives = 424/579 (73%), Gaps = 7/579 (1%)

Query 23   STN-IVAQSQQNRNTNFCSPDSPFSCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARA 81
          STN I AQ8 TNSFC +DSP SctTV Y Aq+P FL + NIS++F S L8IA A
Sbjct 16   STNHIIAQSPATPVTFNFCSTDSPASCTQYVIYAAQAGFLDGNISDLFGISRLSIAFA 75

Query 82   MDNIPVLSNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITVWKPGDNVSLVBDKFGAS 141
          SNL + L D3+LIV+ C CTGN FANT+Y+I DSPFY+ T +ENLIV+ AV
Sbjct 76   SNLIASEARLSPQQLLVPLLCSTGNHYFANITYIKITDDSFYFVSVTFENLITNYNAV 135

Query 142   MDNIPVLSNKLPIGIVQVFFLFCCKPSKNQLDKEIKYLITVWKPGDNVSLVBDKFGAS 206
          INP L P L +G+VVFPLFCCKPSK+ DK I YLITYVW+PGD+V LV AS
Sbjct 136   RALNPGLEPTTLQGVGVVFPFLPCCKPSKSHSDKGINLITYVWQGDQVLLVGTNLKAS 195

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Query 202 PEDIMSENNYQNFATAANLIPVLPVTRLPVLARSPDGRKGIRLPIVIGISLGCITLV 261
Sbjct 196 PDI ENN NF4A+ + PVLIPV4+ P+L+ RG R + + + S G L4
PVDIRDENN-NLNFASVDQVPLIPVSPQPLLTQERRASKG--RWLIALVSTGALLIF 252

Query 262 LVLAIVLVVYVYCLMKTLNRSASSAETAAD--KLISGVSGVYKSPMYETDAIMEATMNLIS 319
Sbjct 253 LVLSILVYGLIRAKKTLDRSSSLZETDILKLLPQSGSYIAKPIVYETVIMAEVWNLN 312

Query 320 RQCKIGRGSYKANIIEKVLAVKFKFDEWTEELKILQKVHNCNLVKLMGVSSDNDGCPVV 379
Sbjct 313 EHYRIGGSVYRATINQVAVKKTEDIETELRIQLQVNBNCNLVKLMGVSSDADGNRFV 372


Query 380 YEYAENGSLDEWLFKSKSCSDTNSRASLTWCQRISMAVDVAMGLQYMHIEAYPRIVHRDI 439
Sbjct 373 YE+AEQSLD+WL K S+ +S+ A LTV QRI +A+DVA GLQYMHIE P +VBRDI
YE+AEQSLD+WLHPKPSBSSSV--AFILTWQRIQVALDVANGILQYMHIEHTQPSVHRDI 431

Query 440 TSNLLIDNDFKAKIANFSMARFTFNRMPEKIDVAFGVVLIILLTGKAKMNTKNGEVV 499
Sbjct 432 +N+LDD FKAKIANFMA N MPEKIDVAFGVVLI+ELLG+KAM + NGEV
TSNLLIDNDFKAKIANFSMARFTFNRMPEKIDVAFGVVLIILLTGKAKMANGEIVE 491

Query 500 MLNKKIDMKIPDQENREERIKKMMOKPESYYPIDVALSLAVNCTADKLSRPTIEA 559
Sbjct 492 MLNKKDIIELEVEDKREDIRRMMDPTLENFYFPGDALNLGLARLCTQKSSARPFMAE 551

Query 560 IVLSISLLTPSPATLERSLTSSGLDVEATQIVTSIAAR 598
Sbjct 552 I+LS+LQ S TLERS E QI+ +AR
IAPNLSVLGQSSSEVIERSGTQGFEPERTIQINPVIAAR 590

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>ref|XP_002533280.1|  serine-threonine protein kinase, plant-type, putative [Ricinus communis]
gb|EEE29112.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
Length=620

GENE ID: 8272992 RCOM 0411680 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]
Score = 638 bits (1645), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 337/603 (55%), Positives = 427/603 (70%), Gaps = 32/603 (5%)

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Query 23 STNIVAGSQQNRNTNFCSPDSSPSCCTVTVYIAQSPNFIALNINIFDTPSILSIARAS 82
Sbjct 23 +T + ADB Q TNFSC D P CTTYV Y AQ PNFL+L NIS+P S ISIA AS
TTYTVTAQSGQ--TNFSCVDLSPSCQTTYVAYYAQPNFNLGNLSDLFVARSILSIARAS 80

Query 83 NLEPMDDKLVQDVLVFPVTCGCTGNRSPANISVEINQDGSFFYVATTSYENLTNWRAM 142
Sbjct 81 NLN D L+ +Q+LLV+TCGCTGN SFANI+Y+I GDSFFV+TT +ENL W+AV
RANVEDIPLMNQLLLVFPVTCGCTGNRSPANITQIKPGDSFFYVATTSYENLAKQAVE 140

Query 143 DLENPFLSPKLPIDIGQVVPFLPCKPCPKRNLQKEIKYLLTYVWKPDGNSVLSDKFGASP 202
Sbjct 141 NFNPNLDPLTFLPGDGVVFPFLPCKPCPKRNLQKEIKYLLTYVWKPDGNSVLSDKFGASP 200

Query 203 PEDIMSENNYQNFATAANLIPVLPVTRLPVLARSPDGRKGIRLPIVIGISLGCITLV 261
Sbjct 201 HDIAIQNNYV--DFSTAVHREPLIPVTPMPLISQSPSPQSRSEHLLVLIIVTSVAGALLI 259

Query 262 LVLAIVLVVYVY--LRMKTILNRSASSAETA--DKLLSG 296
Sbjct 260 FLIVAF+VIAH+CKCKKKKFTVLIHNSLSCLTDLQIQEKGQYRSFEPKILQKLLRCV 319

Query 297 GSVKSPKMYETDAIMEATMNLSECKIGESYKANIIEKVLAVKFKFDEWTEELKILQ 356
Sbjct 320 GSYLCKPIMYDIKEILLATMDLHEHYRIGGSVYRATINQVLAVKKTKVDIETELNLQK 379

Query 357 VNHGNCNLVKLMGVSSDNDGCPVVYEYAENGSLDEWLFKSKSCSDTNSRASLTWCQRISMA 416
Sbjct 380 VNHGNCNLVKLMGVSSDNDGCPVVYEYAENGSLD+WL K + +S+S A L+M QR+ +A
VNHANVLKMGISNNAAGDCFLVYEYAENGSLD+WLHPKPSBSSSVAFLSWSGRQJIA 416



Query 417 VDVAAGLQYMHIEAYPRIVHRDITSNLLIDNDFKAKIANFSMARFTFNRMPEKIDVAF 476
Sbjct 439 LDVAGLQYMHIEAYPRIVHRDITSNLLIDNDFKAKIANFSMARFTFNRMPEKIDVAF 476

Query 477 GVVLIELLTGKAKMNTKNGEVVLMNKKIDMKIPDQENREERIKKMMOKPESYYPIDVA 498
Sbjct 499 GVVLIELLTGKAKMNTKNGEVVLMNKKIDMKIPDQENREERIKKMMOKPESYYPIDVA 498

Query 537 ISLASLVNCTADKLSRPTIEAIVLSISLLTPSPATLERSLTSSGLDVEA-TQIVTSI 595
Sbjct 552 ISLASLVNCTADKLSRPTIEAIVLSISLLTPSPATLERSLTSSGLDVEA-TQIVTSI 595

Query 596 AAR 598
Sbjct 618 IAR 620

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>ref|XP_002310198.1|  predicted protein [Populus trichocarpa]
gb|EEE90648.1|  predicted protein [Populus trichocarpa]
Length=601
GENE ID: 7473142 POPTDRAFT_870366 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 614 bits (1583), Expect = 1e-173, Method: Compositional matrix adjust.
Identities = 328/595 (55%), Positives = 423/595 (71%), Gaps = 17/595 (2%)

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Query 14 LCLVIMFLFSTNIVAGSQQNRNTNFCSPDSSPSCCTVTVYIAQSPNFIALNINIFDTP 73
Sbjct 14 +LV+ +FST +AQ+ TNFSC DSP SC TY+Y+AQ +P+L L IS+P
LFLVLVFFSTVYTAQAPG--TNFSCVDSPSTCPTYISYLAQPPDLDLQKISHLPGI 71

Query 74 SPISIASANLEPMDDKLVQDVLVFPVTCGCTGNRSPANISVEINQDGSFFYVATTSVE 133
Sbjct 72 IASIASANLEPMDDKLVQDVLVFPVTCGCTGNRSPANISVEINQDGSFFYVATTSVE 133

Query 134 NLTMRAVNDINFLVPLSPKLPIDIGQVVPFLPCKPCPKRNLQKEIKYLLTYVWKPDGNSVL 193
Sbjct 134 NLTMRAVNDINFLVPLSPKLPIDIGQVVPFLPCKPCPKRNLQKEIKYLLTYVWKPDGNSVL 193

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Sbjct 132 NLTRMQEVEALNRSLTPTLLHAGDEVIPFLFCCKCPRTHLENGIEHLITYVWQGGDLKK 191

Query 194 VSDKFGASPEDIMSENNGQNTAANNLPVLIPVTRLPVLAR---SPSDGRGGGIRL-IV 249
V+GAKM KES +I+ 2NNY NF AS P+IPV+LVLV +P R+G RI V

Sbjct 192 VAAMLNASENNIYENNY-DNFAAIVNPVIVPSKLVLSQVLYTPE---RSGSKHLIVL 248

Query 250 ITIGSLGCTLLVLVLAVLVVYVC---LKMKTINRSASSAETAD---KLLSGVSVYKSPIM 305
I+ S+ T L L+ C K L+R+ S ET+D KLL GV G+ K +
I+VAAISLSTFTTCLPVAFLLHKRCGYKATKALDRTGSCLETSDFPKLIPGLVGLDKLSII 308

Sbjct 249 I+VAAISLSTFTTCLPVAFLLHKRCGYKATKALDRTGSCLETSDFPKLIPGLVGLDKLSII 308

Query 306 YETDAIMEATMNLSEQCKIGESVYKANIIGKVLAVKRFKEDVTIELKILQVNRHNLVKL 365
YE+DAIME+T+ 2NNY NF AS P+IPV+LVLV +P R+G RI V

Sbjct 309 YELVALEMTDVLHEIYKIGESVYKANIIGKVLAVKRFKEDVTIELKILQVNRHNLVKL 368

Query 366 MCVBSNDND---GNCVFVVEYAENGLDLEWLFKSGSDTNSRAGLFWQRIQMVAIDVAMGL 423
MG+SS+D GN P+VVEYAENGLDLEW LF KS +S+S LFW OR+ +A+DVA GL

Sbjct 369 MCVBSNDSRGNRFLVVEYAENGLDLEWLFKSGSDTNSRAGLFWQRIQMVAIDVAMGL 427

Query 424 QYMEHAYPRIVHRDITSSNILLDSNFKIAKIANFSMARTFTNMMPKIDVFAFGVLLIEL 483
QY+HEH PR+V+DI +SNILLDSNFKIAKIANFSMARTFTNMMPKIDVFAFGVLLIEL
QY+HEHTQPRVHVDITSSNILLDSNFKIAKIANFSMARTFTNMMPKIDVFAFGVLLIEL 487

Sbjct 428 QY+HEHTQPRVHVDITSSNILLDSNFKIAKIANFSMARTFTNMMPKIDVFAFGVLLIEL 487

Query 484 ILGRKAMTITKENGVSVMKIDKRIKIQEENFEERLKKMDPKLESYTPIDVALSGLASIA 543
I+Y GAKM KES +I+ 2NNY NF AS P+IPV+LVLV +P R+G RI V

Sbjct 488 ILGSKAMVTKEKGEIVLICEIKDLEMEERLKKMDPKLESYTPIDVALSGLASIA 547

Query 544 VNCTADKSLRPTARIIVLSILLTPQPRPATLERSLTSGLDVFATQIVTISAAR 596
CT +KS RP+AEIV +I+LQ SP TLER TS +T+V+ +AR

Sbjct 548 RLCTLEKSGRPSMAIIVNLTVLITQSSPETLER-WTSEVTEDFTRLVSPVTAR 601

-emb|CA002936.1 LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=349

Score = 499 bits (1285), Expect = 4e-139, Method: Compositional matrix adjust.
Identities = 248/351 (70%), Positives = 290/351 (82%), Gaps = 4/351 (1%)

Query 54 YIAQSNPFLISITNISNIFDTSPLSIARASNLPEMDKLVKDOVLIVPVTCCTGNRSFAN 113
Y AQSNPFLIS+NIS+IP+ SPL IA+ASN+E D KI+ DQ+LLVVPVTCCT N SFAN

Sbjct 1 YIAQSNPFLISITNISNIFDTSPLSIARASNLPEMDKLVKDOVLIVPVTCCTGNRSFAN 60

Query 114 ISYENGDSQSYFVATTSYENLNRWAVMDLNPVLSFNKLPIDGIVVFLFCCKPSKNOL 173
I+Y I QSD+P+ +I+ 2NNY NF AS P+IPV+LVLV +P R+G RI V

Sbjct 61 ITYSIKGQDNFFILSITSYQNLTYLLEKFNPNPNSPTLLPLDTKVSVPFLFCCKPSKNOL 120

Query 174 DKETIKYLYTYVMKPGDVSLSVSKFGASPEDIMSENNGQNTAANNLPVLIPVTRLPVL 233
+K I KYLYTYVM+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L

Sbjct 121 NKGIKYLITYVMQDNVTLVSSKFGASQVEMLAENNH---NFTASTNRSVLLPVTSLPKL 178

Query 234 ANSPSDGRGGGIR-LPVIITIGISGLCTLLVLVLAVLVVYCLMKTINRSASSAETADKL 292
+S+GRK +I+ I+IGISGL +LVL+ L VYVCLMKT INRS SS+ETADKL

Sbjct 179 QPSNBSGRSSQNLALIGISGLGAFFILVTLVLSIVVYCLMKTINRSASSAETADKL 298

Query 293 LAGVSGVSKPTMYE DAIME TMLNLS CKIGESVYKANI+G+VLAVK+ K+D +EELK 352
L+G VSGVSKPTMYE DAIME TMLNLS CKIGESVYKANI+G+VLAVK+ K+D +EELK

Sbjct 239 LAGVSGVSKPTMYE DAIME TMLNLS CKIGESVYKANI+G+VLAVK+ K+D +EELK 352

Query 353 ILQKVNHNGLVKMLGVSSDNDGNCVFVVEYAENGLDLEWLFKSGSDTNS 403
ILQKVNHNGLVKMLGVSSDNDGNCVFVVEYAENGLDLEWLFKSGSDTNS

Sbjct 299 ILQKVNHNGLVKMLGVSSDNDGNCVFVVEYAENGLDLEWLFKSGSDTNS 348

-emb|CA002948.1 LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=337

Score = 484 bits (1245), Expect = 2e-134, Method: Compositional matrix adjust.
Identities = 238/339 (70%), Positives = 278/339 (82%), Gaps = 3/339 (0%)

Query 49 ETYVYIAQSNPFLISITNISNIFDTSPLSIARASNLPEMDKLVKDOVLIVPVTCCTGN 108
ETVY Y AQSNPFLIS+NIS+IP+ SPL IA+ASN+E D KI+ DQ+LLVVPVTCCT N

Sbjct 1 ETYVYIAQSNPFLISITNISNIFDTSPLSIARASNLPEMDKLVKDOVLIVPVTCCTGN 60

Query 109 SFANITSYENGDSQSYFVATTSYENLNRWAVMDLNPVLSFNKLPIDGIVVFLFCCKP 168
SFANIT+I QSD+P+ +I+ 2NNY NF AS P+IPV+LVLV +P R+G RI V

Sbjct 61 SFANITSYENGDSQSYFVATTSYENLNRWAVMDLNPVLSFNKLPIDGIVVFLFCCKP 120

Query 169 SKNLDKEIKYLYTYVMKPGDVSLSVSKFGASPEDIMSENNGQNTAANNLPVLIPVT 228
SKNLD+K I KYLYTYVM+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT

Sbjct 121 SKNLDKEIKYLYTYVMQDNVTLVSSKFGASQVEMLAENNH---NFTASTNRSVLLPVT 178

Query 229 RLPLVARSBSGRGGGIR-LPVIITIGISGLCTLLVLVLAVLVVYCLMKTINRSASSAET 287
LP L+ +S+GRK +I+ I+IGISGL +LVL+ L VYVCLMKT INRS SS+ETADKL

Sbjct 179 SLPLDQPSNBSGRSSQNLALIGISGLGAFFILVTLVLSIVVYCLMKTINRSASSAET 298

Query 288 TADKLLSGVSVYKPTMYE DAIME TMLNLS CKIGESVYKANI+G+VLAVK+ K+D +EELK 347
TADKLLSGVSVYKPTMYE DAIME TMLNLS CKIGESVYKANI+G+VLAVK+ K+D +EELK

Sbjct 239 TADKLLSGVSVYKPTMYE DAIME TMLNLS CKIGESVYKANI+G+VLAVK+ K+D +EELK 347

Query 348 TEELKILQKVNHNGLVKMLGVSSDNDGNCVFVVEYAENGL 386
+EELKILQKVNHNGLVKMLGVSSDNDGNCVFVVEYAENGL

Sbjct 299 TEELKILQKVNHNGLVKMLGVSSDNDGNCVFVVEYAENGL 337

-emb|CA002942.1 LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=334

Score = 481 bits (1238), Expect = 1e-133, Method: Compositional matrix adjust.
Identities = 237/336 (70%), Positives = 277/336 (82%), Gaps = 3/336 (0%)

Query 54 YIAQSNPFLISITNISNIFDTSPLSIARASNLPEMDKLVKDOVLIVPVTCCTGNRSFAN 113
Y AQSNPFLIS+NIS+IP+ SPL IA+ASN+E D KI+ DQ+LLVVPVTCCT N SFAN

Sbjct 1 YIAQSNPFLISITNISNIFDTSPLSIARASNLPEMDKLVKDOVLIVPVTCCTGNRSFAN 60



Query 114 ISYENGDSQSYFVATTSYENLNRWAVMDLNPVLSFNKLPIDGIVVFLFCCKPSKNOL 173
I+Y I QSD+P+ +I+ 2NNY NF AS P+IPV+LVLV +P R+G RI V

Sbjct 61 ITYSIKQGDNFILSITSYQNLINLYLEKFNPNFNLSPITLLPLDTKVSVPFLCKCPKSNQL 120
 Query 174 DREIKYLIITYVMKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVL 233
 + I IXYLIVPFGD + DNW+LVS KFGAS +++++ENN+ NPTA+ N VLIPPT LP L
 Sbjct 121 NKGIKYLITYVMQDNDVTLVSSKFGASQVEMLAENNH--NFTASTNRSLVLPVTSLEKL 178
 Query 234 ARSPSDGRKGGR+LPIVIGISLGTLLVLVLAVLIVVYVCLMKMTLNRSASAEADKL 292
 + S+GRK + L +IIGISIG +LVL + LVVYVCLMK LNRS SS+ETADKL
 Sbjct 179 DQPSNGRKSQSNLALLIGISGSAFFILVLTLLVYVCLMKMLNRRTSSSETADKL 238
 Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSECKIGESVYKANIEGRVLAVKRFKDETEELK 352
 LSGVSGYVSKPTMYETDAIMEATMNLSECKIGESVYKANIEGRVLAVKRFKDETEELK
 Sbjct 293 LSGVSGYVSKPTMYETDAIMEATMNLSECKIGESVYKANIEGRVLAVKRFKDETEELK 352
 Query 353 ILQKVNHNGLVKIMGVSSDNDGNCFFVVEYAENGSL 388
 ILQKVNHNGLVKIMGVSSDNDGNCFFVVEYAENGSL
 Sbjct 299 ILQKVNHNGLVKIMGVSSDNDGNCFFVVEYAENGSL 334

>emb|CA002960.1 LyeM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=333

Score = 477 bits (1228), Expect = 2e-132, Method: Compositional matrix adjust.
 Identities = 235/335 (70%), Positives = 275/335 (82%), Gaps = 3/335 (0%)

Query 54 YIAQSPNPLSLTNISNIFDPSLIARASNLPEMDKLVKQDVLVLPVTCCTGNRSFAN 113
 Y AQSPNPLSLTNISNIF+ SPL IA+ASN+E D KL+ DQ+LLVPTVTCCT N SFAN
 Sbjct 1 YRAQSPNPLSLTNISNIFNLSPILRIKASNLIAEKDKLLPQQLLVLPVTCCTGNRSFAN 60
 Query 114 LSGVEINGDSFYFVATTSEYNLTNWRVMDINPVLSPNKLPIGIVFPLCKCPKSNQL 173
 +IV I GGD+P + + TSNLNTN+ + NP LSP LP+ +V PLFCPCPKSNQL
 Sbjct 61 ITYSIKQDNFILTYSIQNLINLYLEKFNPNFNLSPITLLPLDTKVSVPFLCKCPKSNQL 120
 Query 174 DREIKYLIITYVMKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVL 233
 +R IXYLIVPFGD + DNW+LVS KFGAS +++++ENN+ NPTA+ N VLIPPT LP L
 Sbjct 121 NKGIKYLITYVMQDNDVTLVSSKFGASQVEMLAENNH--NFTASTNRSLVLPVTSLEKL 178
 Query 234 ARSPSDGRKGGR+LPIVIGISLGTLLVLVLAVLIVVYVCLMKMTLNRSASAEADKL 292
 + S+GRK + L +IIGISIG +LVL + LVVYVCLMK LNRS SS+ETADKL
 Sbjct 179 DQPSNGRKSQSNLALLIGISGSAFFILVLTLLVYVCLMKMLNRRTSSSETADKL 238
 Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSECKIGESVYKANIEGRVLAVKRFKDETEELK 352
 LSGVSGYVSKPTMYETDAIMEATMNLSECKIGESVYKANIEGRVLAVKRFKDETEELK
 Sbjct 293 LSGVSGYVSKPTMYETDAIMEATMNLSECKIGESVYKANIEGRVLAVKRFKDETEELK 352
 Query 353 ILQKVNHNGLVKIMGVSSDNDGNCFFVVEYAENGSL 387
 ILQKVNHNGLVKIMGVSSDNDGNCFFVVEYAENGSL
 Sbjct 299 ILQKVNHNGLVKIMGVSSDNDGNCFFVVEYAENGSL 333

>ref|XP_002468236.1  hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]
gb|EER95234.1  hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]
 Length=631

GENE ID: 8085264 SORBIDRAFT_01g042230 | hypothetical protein [Sorghum bicolor]
 (10 or fewer PubMed links)

Score = 441 bits (1133), Expect = 2e-121, Method: Compositional matrix adjust.
 Identities = 256/589 (43%), Positives = 352/589 (59%), Gaps = 57/589 (9%)

Query 32 QDRNTNFSC-----SDPPCEITYVYIAQSPNPLSLTNISNIFDPSLIARASNL 84
 QDN TN+ P S SPP C+TVY QBP + L +I+H+P TS IA A+ L
 Sbjct 22 QDN TNVYVQAQPCACNVSSESPPC+TVYVYVYRQCYQDGLSLPDTGQARLASNGV 80
 Query 85 EPMDKLVKQDVLVLPVTCCTGNRSFANISYEINGDSFYFVATTSEYNLTNWRVMD 143
 D + I LVEP+ GCGTQ SFAN+Y I QGD+P+ +A SEYNLT ++ +
 Sbjct 81 SSEGDVQLGQPLVLPVSKCGCTGWSFANVYPIRGDTFFLNARVSYENITLYQLIQN 140
 Query 144 LNPVLSNKLPIGIVQVFFPLCKCPKSNQLDEIKYLIITYVMKPGDNVSLVSDKFGASPE 203
 INP P L +G +V PLTC+CP+ E ITVVM+ GD +S VS + +
 Sbjct 141 LNPASVPTSLGVQGVTVLPFLFCRCFAP----ARSSFTIVYVQAGDTMSVSKLMNTED 196
 Query 204 DIMSENNYQNFATAANN--NLPLVLPVTRLPVL-----ARSPSDGRKGGRILPVLIPVIGISIG 256
 + I NN + +A+L +E+LTP +P L A S DG+ R VILG S+
 Sbjct 197 ETEAANNVTSSASNLASGLPMLIFVQPRPLFLYLAASAGDKSRWRRAVIGASVS 256
 Query 257 CTLVLVLAVLIVVYVCLK-----MKTLNRSASASAE----- 287
 + V+ IAL V L+ L+ M+ +R A + + +
 Sbjct 257 GS--VVALAALFVAILARRYKPKSPMLGSRFVANTKLTWSNRQFGHSDNSFAMMKL 314
 Query 288 TADKLLSGVSGYVSKPTMYETDAIMEATMNLSECKIGESVYKANIEGRVLAVKRFKDE 347
 KGL+VSS+ ++ R+ + + IMEATMNL E+CKIG + Y+A ++G+V AVK K DV
 Sbjct 315 KGLVLLVSSPTDK+ITLEETSEATMNLDECKIGESTYKRLKLDGVFAVKRPAKGDV 374
 Query 348 TEELKILQKVNHNGLVKIMGVSSDNDGNCFFVVEYAENGSLDEWLFSEKSCDTSNR-- 404
 EIK+Q VNR NL+ G+S DG+ FVVE+AS GRDML+ R S +S
 Sbjct 375 SAELNRMVMNHNGLIKLAGISIGTDGDAFLVVEFAEKGLDKWLYKPPSLPSSSC 434
 Query 405 --ASLTWCORTSMVAVDAMGLQYMHAEYHPRVHRDITSSNILLSDNFKAFIANTFSMAR- 461
 A+L+W QR+S+A+DVA GL YMHHE P +VH DI + NILL + E+ KI+ FS+A+
 Sbjct 435 TVATLSWQRLSLADLVANGLLYMHHEHTQPSMVHGDIRARNLLTAEFRKISGFSGLK 494
 Query 462 TFPNPMMPKILDVAPGVVLELTLGRAMKTTENGSEVVMWKIDWKIFDQENRDEELK 521
 + + DVAP++L+ELLA+GRAM + + E+ MDM+I + D + R+L+K
 Sbjct 495 ATADAAATSSVFAPGLLELLELLSGRAMRARSVSEIQMLMREIRGVLDAGKREAKLGK 554
 Query 522 WNDDPKSEYYPIDYIALSLALVNC+TACKSLARPTTIAVILSLITQP 570
 WNDD L S Y +D ALSIA +A CT D + R+ +E+V SL+L QP
 Sbjct 555 WNDDPALGSEYHMDALSLAGMARACTEDDAARRNMTVEVFSVLVQOP 603

>emb|CA002953.1 LyeM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=313

Score = 436 bits (1120), Expect = 6e-120, Method: Compositional matrix adjust.

Identities = 216/315 (68%), Positives = 255/315 (80%), Gaps = 3/315 (0%)

```

Query 54 YIAQSPNFIISLTNINISNIFDTSPLSIARASNLBMDKRLVKDQVLLVPVTCCTGCTNRGSFAN 113
      Y AQSBNFISLISNIDIFNLSPRIARASNLBMDKRLVKDQVLLVPVTCCTGCTNRGSFAN
Sbjct 1 YRAQSPNFIISLTNINISNIDIFNLSPRIARASNLBMDKRLVKDQVLLVPVTCCTGCTNRGSFAN 60

Query 114 ISVEINQDGSFYVATTSEYENLTNRKAVMDINPVLSPNKLPIGIVQVFFLPCKCPCKSNQ 173
      I+Y I QSD+T+ + TSV+NLTN+ + NP LSP LP+ +V PLFCCKCPCKSNQ
Sbjct 61 ITYSIKQDGNFILTSTSYQNLNLYLEPKFNPNPNSPTLLPLDTKVSVPFLFCCKCPCKSNQ 120

Query 174 DKXIKYLIITYVMKPGDNVSLVSKFGASPEDIMSENNYQGNFTANNLPVLIPVTRLEVL 233
      +K IKYLIITYVM+ DN+LVS KEGAS +++ENNA+ NFTA+ M VLIIVT LP L
Sbjct 121 NKGIKYLIITYVMQDNDVTLVSSKFGASQVEMLAENNA--NFTASTNRSLVLPVTSLEKL 178

Query 234 ARSPSDGRKGGIR-LPVIIGISIGCTLLVLVLAVLIVVYVCLMKLNRSASASATADKL 292
      + SGRK + L +IIGISIG +VL+ LVVYVCLMK LNRS SS+ETADKL
Sbjct 179 DQPSNDRKSGSSQNLALLIGISLGSAAFFILVTLISLVVYVCLMKLNRSSTSSATADKL 238

Query 293 LSGVSGYVSKPMYETDAIMEATMNLSECKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
      LSGVSGYVSKPMYET DAIME T NLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPMYETDAIMEATMNLSDCKIGESVYKANIDGRVLAVKRIKADASELK 298

Query 353 ILQKVNHNKLVKLMG 367
      ILQKVNHNKLVKLMG
Sbjct 299 ILQKVNHNKLVKLMG 313

```

>emb|CA002964.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 emb|CA002964.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=311

Score = 433 bits (1113), Expect = 4e-119, Method: Compositional matrix adjust.
 Identities = 215/313 (68%), Positives = 254/313 (81%), Gaps = 3/313 (0%)

```

Query 54 YIAQSPNFIISLTNINISNIFDTSPLSIARASNLBMDKRLVKDQVLLVPVTCCTGCTNRGSFAN 113
      Y AQSBNFISLISNIDIFNLSPRIARASNLBMDKRLVKDQVLLVPVTCCTGCTNRGSFAN
Sbjct 1 YRAQSPNFIISLTNINISNIDIFNLSPRIARASNLBMDKRLVKDQVLLVPVTCCTGCTNRGSFAN 60

Query 114 ISVEINQDGSFYVATTSEYENLTNRKAVMDINPVLSPNKLPIGIVQVFFLPCKCPCKSNQ 173
      I+Y I QSD+T+ + TSV+NLTN+ + NP LSP LP+ +V PLFCCKCPCKSNQ
Sbjct 61 ITYSIKQDGNFILTSTSYQNLNLYLEPKFNPNPNSPTLLPLDTKVSVPFLFCCKCPCKSNQ 120

Query 174 DKXIKYLIITYVMKPGDNVSLVSKFGASPEDIMSENNYQGNFTANNLPVLIPVTRLEVL 233
      +K IKYLIITYVM+ DN+LVS KEGAS +++ENNA+ NFTA+ M VLIIVT LP L
Sbjct 121 NKGIKYLIITYVMQDNDVTLVSSKFGASQVEMLAENNA--NFTASTNRSLVLPVTSLEKL 178

Query 234 ARSPSDGRKGGIR-LPVIIGISIGCTLLVLVLAVLIVVYVCLMKLNRSASASATADKL 292
      + SGRK + L +IIGISIG +VL+ LVVYVCLMK LNRS SS+ETADKL
Sbjct 179 DQPSNDRKSGSSQNLALLIGISLGSAAFFILVTLISLVVYVCLMKLNRSSTSSATADKL 238

Query 293 LSGVSGYVSKPMYETDAIMEATMNLSECKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
      LSGVSGYVSKPMYET DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPMYETDAIMEATMNLSDCKIGESVYKANIDGRVLAVKRIKADASELK 298

Query 353 ILQKVNHNKLVK 365
      ILQKVNHNKLVK
Sbjct 299 ILQKVNHNKLVK 311

```

>emb|CA002944.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 var. truncatula
 Length=307

Score = 427 bits (1097), Expect = 2e-117, Method: Compositional matrix adjust.
 Identities = 211/309 (68%), Positives = 250/309 (80%), Gaps = 3/309 (0%)

```

Query 54 YIAQSPNFIISLTNINISNIFDTSPLSIARASNLBMDKRLVKDQVLLVPVTCCTGCTNRGSFAN 113
      Y AQSBNFISLISNIDIFNLSPRIARASNLBMDKRLVKDQVLLVPVTCCTGCTNRGSFAN
Sbjct 1 YRAQSPNFIISLTNINISNIDIFNLSPRIARASNLBMDKRLVKDQVLLVPVTCCTGCTNRGSFAN 60

Query 114 ISVEINQDGSFYVATTSEYENLTNRKAVMDINPVLSPNKLPIGIVQVFFLPCKCPCKSNQ 173
      I+Y I QSD+T+ + TSV+NLTN+ + NP LSP LP+ +V PLFCCKCPCKSNQ
Sbjct 61 ITYSIKQDGNFILTSTSYQNLNLYLEPKFNPNPNSPTLLPLDTKVSVPFLFCCKCPCKSNQ 120

Query 174 DKXIKYLIITYVMKPGDNVSLVSKFGASPEDIMSENNYQGNFTANNLPVLIPVTRLEVL 233
      +K IKYLIITYVM+ DN+LVS KEGAS +++ENNA+ NFTA+ M VLIIVT LP L
Sbjct 121 NKGIKYLIITYVMQDNDVTLVSSKFGASQVEMLAENNA--NFTASTNRSLVLPVTSLEKL 178

Query 234 ARSPSDGRKGGIR-LPVIIGISIGCTLLVLVLAVLIVVYVCLMKLNRSASASATADKL 292
      + SGRK + L +IIGISIG +VL+ LVVYVCLMK LNRS SS+ETADKL
Sbjct 179 DQPSNDRKSGSSQNLALLIGISLGSAAFFILVTLISLVVYVCLMKLNRSSTSSATADKL 238

Query 293 LSGVSGYVSKPMYETDAIMEATMNLSECKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
      LSGVSGYVSKPMYET DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPMYETDAIMEATMNLSDCKIGESVYKANIDGRVLAVKRIKADASELK 298

Query 353 ILQKVNHN 361
      ILQKVNHN
Sbjct 299 ILQKVNHN 307

```

>gb|JAM19130.1|AC103891.10 Putative protein kinase [Oryza sativa Japonica Group]
 gb|ABF94815.1| Protein kinase domain containing protein [Oryza sativa (Japonica cultivar-group)]
 gb|EA226175.1| hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]
 Length=624

Score = 426 bits (1096), Expect = 3e-117, Method: Compositional matrix adjust.
 Identities = 251/600 (41%), Positives = 355/600 (59%), Gaps = 43/600 (7%)

```

Query 10 LHSQILGLIVMLFSTNIVAGAGQGDNR-----NFCSPSDSPSCCTVYVYIAGSPNFIISLT 65
      + L2+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 1 MEHKGCLILAVIAPLAGAEAVTDATARRRFACNVSAP--COTFVYVYVYVYVYVYVYVYVYVYV 58

Query 66 NISNIFDTSPLSIARASNLBMDKRLVKDQVLLVPVTCCTGCTNRGSFANIEGKVLAVKRFKEDVTEELK 125
      NIS+H+ S IA+ L D L+ Q LILVP CGCTG RSFAN+Y I D+H+

```

Sbjct 59 NISDLFGVGRALLASANKLTEDGVLLPQGPLLVFVKCGCTGARSFANVTYPIRPROTF 118

Query 126 FVATTSYENLNWRVMDLNPVLSNPKLPIGIQVFPPLCKPSKQDLKEIKYLITYVM 185
+A T++ENL++ V +NP +L +VV PLFC+CP++ +L +L+TVVM
Sbjct 119 GLAVTAFENLTDVFLVEELNPAEATRLPEWQGVVPLFCRCPTREEISAGSRLLATVYM 178

Query 186 KPGDNVLSVSKDGASPEDIMSENNYQNTAANNLPVLPVTRP-----VLARP 237
+PGD+VS+VS AS ++ +N N ± A PVLIFV+ P +A P
Sbjct 179 QPGDVSVSALMNASAAANLASNGVAGNSTFATGQGVLLPVSQGPRFFPLTYGAIADP 238

Query 238 SDG--RKGGRIRLPVIGISGCTLLVLVLAVLLVYVYCLMK-----KTINRS 282
+G R +Y K C VL +A L Y K +KNR
Sbjct 239 GAGKHRRHIIWATSISAGSFVACA--VLTALAYRYRKKAFVKPHVSPKLSWTKSLNRF 296

Query 283 ASSAETA-----DKLLSGCVSYSKPTMYETAIMEATMNLSEQCKIGESVYKANIEGK 336
S++ A DKLL+ VS ++ KP ++ + IMEATMNL ECKG+G S Y+AN+E +
Sbjct 297 DNSSIARMINGGDKLLTSVSQFDKFIIFREEIMEATMNLSEQCKIGSSYRANLRE 356

Query 337 VLAVRKFKEDVTEELKILQVNHGKLVKMGVSSNDGN-CFVYVEAENGSLDEWLFSE 395
V AVK K +V EL++Q VNH NL KL G+S DG+ F+VVE+AE GSD+WL+ K
Sbjct 357 VFVAVKPAKONVAGELRMQVNHANLTKLAGISGADGQYAFIYVEFAEGSLDKWLYK 416

Query 396 SCSDTSNRS--ASLTWQRIAMAVDAMGLQYMHAYPRIVHRDITSSNLLDSNFKAK 453
+S +S A++M GR+ A+DVA GL Y+HEH P +VE D+ +NLL + F+AK
Sbjct 417 PPCSQSSSSVATLSWDKRLGLDALVANGLLYLRHTQPSMVHGDVVRANILLTAGFRA 476

Query 454 IANFSMAR--FTTNPMMPKIDVPAFGVLIETLGRKAMTTKENGVEVLMKDKIKFIDQ 511
++NFS+A+ + DVATFG+L+ELL+GR+A+ +E +ML +I +D
Sbjct 477 LSNFLSLAKFAMVDAATSSDVFAGLLLELLSGRVAVRAGVEIGMIRTIARTVDA 536

Query 512 -EENREERLKKMDFPKLSYYPIDVALSLASLAVNCTADKLSRPTIAEIVLSLSLTP 570
+R +L+KMDP L Y +D ALSIA +A CT + + RF +AEI SLS+L QP
Sbjct 537 GQDKRAAKLRKMDPTLGEYGVDAALSISAGRACTEEDAAERPKMAEIAFSLVLSQGP 596

>gb|EAY89155.1| hypothetical protein Os1_10648 [Oryza sativa Indica Group]
Length=624

Score = 426 bits (1094), Expect = 6e-117, Method: Compositional matrix adjust.
Identities = 251/600 (41%), Positives = 355/600 (59%), Gaps = 43/600 (7%)

Query 10 LHSQILCLVILNFTSNIVAGSQDNRT---NFSPCSDBSPSCSTYVTVYIAQSPNFSLT 65
+ + LC++ ++ + + + T F+C +P C T+V Y QSP FL L
Sbjct 1 QHLKGLCILAVFIQALGGQAVTDAFARRAFACNVSPA--CDTTFVYVYQSPGFLIDG 58

Query 66 NISNIFDTPSLIARASNLDPMDKLVKDDVLVFPVTCGTGNRSFANISYEINGDSFY 125
NIS+ S R TA A L D L+ Q CQCG CSKAF++Y I +P+
Sbjct 59 NISDLFGVGRALLASANKLTEDGVLLPQGPLLVFVKCGCTGARSFANVTYPIRPROTF 118

Query 126 FVATTSYENLNWRVMDLNPVLSNPKLPIGIQVFPPLCKPSKQDLKEIKYLITYVM 185
+A T++ENL++ V +NP +L +VV PLFC+CP++ +L +L+TVVM
Sbjct 119 GLAVTAFENLTDVFLVEELNPAEATRLPEWQGVVPLFCRCPTREEISAGSRLLATVYM 178

Query 186 KPGDNVLSVSKDGASPEDIMSENNYQNTAANNLPVLPVTRP-----VLARP 237
+PGD+VS+VS AS ++ +N N ± A PVLIFV+ P +A P
Sbjct 179 QPGDVSVSALMNASAAANLASNGVAGNSTFATGQGVLLPVSQGPRFFPLTYGAIADP 238

Query 238 SDG--RKGGRIRLPVIGISGCTLLVLVLAVLLVYVYCLMK-----KTINRS 282
+G RGI I G C VL +A L Y K +KNR
Sbjct 239 GAGKHRRHIIWATSISAGSFVACA--VLTALAYRYRKKAFVKPHVSPKLSWTKSLNRF 296

Query 283 ASSAETA-----DKLLSGCVSYSKPTMYETAIMEATMNLSEQCKIGESVYKANIEGK 336
S++ A DKLL+ VS ++ KP ++ + IMEATMNL ECKG+G S Y+AN+E +
Sbjct 297 DNSSIARMINGGDKLLTSVSQFDKFIIFREEIMEATMNLSEQCKIGSSYRANLRE 356

Query 337 VLAVRKFKEDVTEELKILQVNHGKLVKMGVSSNDGN-CFVYVEAENGSLDEWLFSE 395
V AVK K +V EL++Q VNH NL KL G+S DG+ F+VVE+AE GSD+WL+ K
Sbjct 357 VFVAVKPAKONVAGELRMQVNHANLTKLAGISGADGQYAFIYVEFAEGSLDKWLYK 416

Query 396 SCSDTSNRS--ASLTWQRIAMAVDAMGLQYMHAYPRIVHRDITSSNLLDSNFKAK 453
+S A++M GR+ A+DVA GL Y+HEH P +VE D+ +NLL + F+AK
Sbjct 417 PPCSQSSSSVATLSWDKRLGLDALVANGLLYLRHTQPSMVHGDVVRANILLTAGFRA 476

Query 454 IANFSMAR--FTTNPMMPKIDVPAFGVLIETLGRKAMTTKENGVEVLMKDKIKFIDQ 511
++NFS+A+ + DVATFG+L+ELL+GR+A+ +E +ML +I +D
Sbjct 477 LSNFLSLAKFAMVDAATSSDVFAGLLLELLSGRVAVRAGVEIGMIRTIARTVDA 536

Query 512 -EENREERLKKMDFPKLSYYPIDVALSLASLAVNCTADKLSRPTIAEIVLSLSLTP 570
+R +L+KMDP L Y +D ALSIA +A CT + + RF +AEI SLS+L QP
Sbjct 537 GQDKRAAKLRKMDPTLGEYGVDAALSISAGRACTEEDAAERPKMAEIAFSLVLSQGP 596

>emb|CAO02946.1| LyeN-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=305

Score = 422 bits (1095), Expect = 6e-116, Method: Compositional matrix adjust.
Identities = 209/307 (68%), Positives = 248/307 (80%), Gaps = 3/307 (0%)

Query 54 YIAQSPNFSLTNISTNIFDTPSLIARASNLDPMDKLVKDDVLVFPVTCGTGNRSFAN 113
Y AQSPNFSLT+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LVLVFPVTCGTGNRSFAN
Sbjct 1 YIAQSPNFSLTNISTNIFDTPSLIARASNLDPMDKLVKDDVLVFPVTCGTGNRSFAN 60

Query 114 ISYEINGDSFYFVATTSYENLNWRVMDLNPVLSNPKLPIGIQVFPPLCKPSKQDLKEIKYLITYVM 173
I+I QGD+P++ TSY+NLN+ + NP LSP LB+ +V PLCKPSKQDLKEIKYLITYVM
Sbjct 61 IYIAQSPNFSLTNISTNIFDTPSLIARASNLDPMDKLVKDDVLVFPVTCGTGNRSFAN 120

Query 174 DKEIKYLITYVMQPGDNVLSVSKDGASPEDIMSENNYQNTAANNLPVLPVTRPVL 233
L +L++NN+ NFA+ N VLPVTRP
Sbjct 121 NKGIKYLITYVMQDNVNLVSKRSGASQVEMLAENH--NFTASTNRSLVLPVTSLEKL 178

Query 234 ARSPDRGKGRIR-LPVIIGISGCTLLVLVLAVLLVYVYCLMKTLNRSASSAETADKL 292
+S+GRK +L +IGISG +LVL +LVYVYCLMK LNRS SS+ETADKL
Sbjct 179 DQPSNGRKSQSNALLIGISIGSAFFLVLTLVLVYVYCLMKLRNRSASSAETADKL 238

Query 293 LSGSVGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIEGKVLAVRKFKEDVTEELK 352
LSGSVGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIEGKVLAVRKFKEDVTEELK
Sbjct 239 LSGSVGVSKPTMYETAIMEATMNLSEQCKIGESVYKANIEGKVLAVRKFKEDVTEELK 298

Query 353 ILQKVN 359
 ILQKVN
 Sbjct 299 ILQKVN 305

>emb|CA002962.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=304

Score = 418 bits (1075), Expect = 9e-115, Method: Compositional matrix adjust.
 Identities = 208/306 (67%), Positives = 247/306 (80%), Gaps = 3/306 (0%)

Query 54 YIAQSPNFIISNTISNIFDTPSLISARASNLPEMDKLVKDVLPVPTCCCTGPNRIFAN 113
 Y AQSPEFIISNTISNIFDTPSLISARASNLPEMDKLVKDVLPVPTCCCTGPNRIFAN
 Sbjct 1 YIAQSPNFIISNTISNIFDTPSLISARASNLPEMDKLVKDVLPVPTCCCTGPNRIFAN 60

Query 114 ISYEINQDSYFYVATTSEYENLNWRAVMDLNPVLSFNKLPICGVVPEFLCKCPKSNQ 173
 I+Y I QGD+T++ TS+NLN+ + NP LSP LP+ +V PLCKCPKSNQ
 Sbjct 61 ITYSIKQGNFISITSYQNLINYLEKPNFNPISPTLLPLDTVSVPLFCCKCPKSNQ 120

Query 174 DKRIKYLITYVVKPGDQVSLVSDKFGASPEDIMSENNYQNFNTAANNLPVLPVTRLE 233
 +K IXYLITYVW+ DN+LVS KEGAS +++ENN+ NFTA+ N VLPVTP LP L
 Sbjct 121 NKGITLITYVQDNQNVLSVSKFGASQVMAENLN+ NFTA+NNRVLVLPVTRLE 178

Query 234 ARSPSDGRKGGIR-LPVIIGISLQCTLLVLVLAVLLVYVYCLMKTIINRBSASATADKL 292
 +S+GRK +L+IGISLQ +LVL+ LVYVYCLMK IAR S+VADKL
 Sbjct 179 DQPSNNGRKSQNLALLIGISLSAFTLVLTLLVYVYCLMKRIINRSTSSATADKL 238

Query 293 LSGSVGVSKPTMYETDAIMEATMNLSEQCIGESVYKANIEGVLAVKRFKEDETRLEK 352
 LSGSVGVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
 Sbjct 239 LSGSVGVSKPTMYETDAIMEATMNLSDNCKIGESVYKANIDGRVLAVKRIKADASELK 298

Query 353 ILQKVN 358
 ILQKVN
 Sbjct 299 ILQKVN 304

>ref|XP_002517029.1| G serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 gb|EF45192.1| G serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 Length=615

GENE ID: 8280185 RCOM 0909430 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 366 bits (939), Expect = 5e-99, Method: Compositional matrix adjust.
 Identities = 216/566 (38%), Positives = 324/566 (57%), Gaps = 65/566 (11%)

Query 48 CEYVYVYIAQSPNFIISNTISNIFDTPSLISARASNLPEMDKLVKDVLPVPTCC-- 105
 C+T L Y VPA+P+L I++ +H+ S L T+ SN+ L+ +Q L VPA+ C
 Sbjct 44 CQTYAFYAPMAPNFDLADSLVGSDFSVSRIMISEPNSISSPSPPLPNQSLFVPSISCA 103

Query 106 ---TGNRSPANISYEINQDSYFYVATTSEYENLNWRAVMDLNPVLSFNKLPICGVVPE 162
 T N S+AN+SY I + D+FY V+T +NL+ +AV +NP L P L IG +V+P
 Sbjct 104 INSTNLSEYANLSEYIKDDTFYLVSTQFNLTQYQVQVNPVLPVLTLEIGQEVIFP 163

Query 163 LFCCKPKNQDKEIKYLITYVVKPGDQVSLVSDKFGASPEDIMSENNYQNFNTAANNLP 222
 +ECPK+ +Q L++ ++I+V++P DN+SLV+ EG + I+ N G N
 Sbjct 164 VECCKPQVQLQVQVNPVSVYVQPSNLSDASSETQCTGSDVWV---DNVQPTDT-- 219

Query 223 VLPVTRLEVLARS---PSDGRKGGIRLPVIIGISLQCTLLVLVLAVLLVYVYCLMKTL 279
 ++HV RLP I++ PS + R +T G++G +L I++ + + L
 Sbjct 220 IFVFNRLPQLSQPVVPSVPTKEKRRGLITGLAVGLGVCGLL-LIIGSMWFREGKL 278

Query 280 NRASAS -----ATADEKLLSGVSGVSKPTMYETDAIMEATMNLSEQC 322
 NR S E KL++ VS + K +++ D +EAT +E
 Sbjct 279 NRKKSSEDEKRLRFYKGEKGLTETMETKLADVSDCLQYRVFKIDELKATDGFNF 338

Query 323 KIGESVYKANIEGVLAVKRFKEDETRLEKILQKVNHGNLVKMGVSSDN-DGCGPVVYE 381
 +SVK +S+ A+K+ K + EELKILQKVNHGNLVK G D+ DG+C++YE
 Sbjct 323 LIGSVYKSGINSQDYALKKKNMAYEELKILQKVNHGNLVKRGFCIDSGSCYLIYE 398

Query 382 YAKNSGLDEWLFKSCSDTSNRASLTQWQRCISMAVQVAMGLQYHEHAYPRIVHDRTS 441
 Y ENGL M L N L W R +A+DVA GLQY+HER PR+VR+DI S
 Sbjct 399 YIENGSLHSMH-----INKNEKLNKRLRIADVANGLOYIHEHTRPRVVKHDKIS 451

Query 442 SNLLIDSNFKAKIANFEMARFTTNMM-----PKIDVEAFGVVL 480
 SNLLIDS +AKIANF+A+ N + +DVF+FGVVL
 Sbjct 452 SNLLIDSNFKAKIANFGLAKSGCNALTMHVITQGYIAPEYLTGQVSTMDVPSFGVVL 511

Query 481 TELLTGRKANTKENGVEVLMKDIKIFD-GENEERILKWMKP-L-LESTYPIIDVALS 538
 +T+G+R+P G+ V V LM + +D+ EB + +RIK MD L +
 Sbjct 512 LELISKEAI--DEEGRV--LMAKVGSGWQNEKKVRLKGMFDESLLRSCSMESI 567

Query 539 LASLAVNCTADKLSRPTIARIVLSL 564
 ++AV C R2++ +IV L
 Sbjct 568 VNNVAVACLAKDPKRRPMVDIVYDL 593

>ref|XP_002280070.1| G PREDICTED: hypothetical protein [Vitis vinifera]
 Length=622

GENE ID: 100264758 LOC100264758 | hypothetical protein LOC100264758 [Vitis vinifera]

Score = 355 bits (912), Expect = 8e-96, Method: Compositional matrix adjust.
 Identities = 220/589 (37%), Positives = 329/589 (55%), Gaps = 68/589 (11%)

Query 28 AQSQ-QNNNTFSQPSD-SFSCCEYVYVYIAQSPNFIISNTISNIFDTPSLISARASNL 85
 +Q+ S L T+ Y A SPNFI I++ +P S L T+ SN
 Sbjct 27 SQAQEPENATQYPSANLSYCHTFATYFASNFEDLALICIDVLSYRIMISEPNIS 86

Query 86 PMDKLVKDVLPVPTCC-----TGNRSPANISYEINQDSYFYVATTSEYENLNWRA 140
 + LV Q L VPA+ C C T S+AN+SY I GD+FY VIT S I NL+ + +

Sbjct 87 SPBNPLVAGQSLFVPLNCSCNSVNTTATISYANLSYTIKSGDTFFLVSTFSLNLTYYYS 146

Query 141 VMDNLVPLSNPKLPIGIVQVFFLCKPCPKSNQDREIKYLVITVMKPGDNVSLVSDKFGA 200
V +NS I P L +G +V+P+P+CKCP+ GL + L I +V+P DM+ + V+ G+
Sbjct 147 VEIVNPTLVPTDLDGDKVIFPFCCKPNETQLANGVNLISYVEQSDNLTGVAASLGS 206

Query 201 SPEDIMSENNYQNPATANNLPVLIPVTRLP-----VLARSFSDGRKGGRILPVIIGIS 254
I+ N G N + +PV+RLP V A + R K R VIIG+
Sbjct 207 DTASIIDVN--GDNIQEFT--IFVPSRLPNISQPNVTASVATSVKVE--RKGVIIGLA 261

Query 255 LG--CILLVILVAVLLVYVYCI--KMKTL-----NRSASSAETADKLLSGVSGV 300
+ G L L + C + K A K + L + + VS +
Sbjct 262 LGIGAGLILLVLLIGVWYRHYVMVEIKETEGDKERPLVGRGTGLKAEVNMADVBDCL 321

Query 301 SKPTMYETDAIMEATNLSQCKIGESVYKANIECKVLAVKREKEDVTEELKILQKVNHG 360
R +Y + + +AT SE I SVK IIG+ A K + K + EELKILQKVNHG
Sbjct 322 DKYKYGIEELRDATGFSERSLILQSVYKGSIDGELYAIKMKWYAEELKILQKVNHG 381

Query 361 NLVKMGVSSD--NDGNCFFVVEYAENGSLDEMLFSKSCSDTSNRSASLTWQORISMAVIV 419
NLV+ L G D D C +VYE+ ENGL WL + L W R+ + +A+V
Sbjct 382 NLVLEGGFIDPEDATCYLVEFVINGSLQWLH-----GDRDEKLNWNRIRIADIV 434

Query 420 AMGLQWMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTPTNPM----- 468
A GLQY+HEE PR+VH+DI SENLILD N +AKIAN +A+ + I +
Sbjct 436 AMGLQYIHEHTRPRVHKIDKSNILLDGNMRKIANFGLAKSGCNALTMHIVGTQGYIA 494

Query 469 -----PKIDVFAPGVVLIETLGRKAMTTKNGEVVMIKKDKIFD--QENRE 516
+DVF+FGVVL+EL+G+G+A+ E G V LW I + E + +
Sbjct 495 PEYLDAGGVSTMDVFSFGVVLLEISGKAEV--DEGRV--LAMSARGILEGKDEKVKVA 550

Query 517 ERLKMDMKPR-LESYYPIDYALSIASLAVNCTADKLSRPTAIVLSL 564
+R+K RMD L +D +D + +A CT RPA+ +IV +L +
Sbjct 551 KKKVMDDEGLLRESCMSNVINWAVATACTHRDPSKRPBMVDIVYAL 599

>gb|AA00791.1| SYM10-like protein [Galega orientalis]
Length=244

Score = 351 bits (901), Expect = 2e-94, Method: Compositional matrix adjust.
Identities = 179/244 (73%), Positives = 204/244 (83%), Gaps = 3/244 (1%)

Query 223 VLIPVTRLEVLARSFSDGRKGGRIL-LEPVIIGISLGLTLLVILVAVLLVYVYCKMKPTLR 281
+LIPV LP L + S G + LEVIGISLG +VL+ LVYVYCKMKR LNR
Sbjct 1 LIPVTRLEPKLDGSSGSSISSSKLLPVIIGISLGAFFIVVILVLSLVYVYCKMKR 400

Query 282 SASASAEADKLLSGVSGVSKPTMYETDAIMEATNLSQCKIGESVYKANIECKVLAVK 341
S ASAEADKLLSGVSGVSKPTMYE D IMEAT +IG+QCKIGESVYKAN+ + LAVK
Sbjct 61 STSLAETADKLLSGVSGVSKPTMYEIDVIMEATNLSQCKIGESVYKANIDSRDLAV 120

Query 342 RFKEDVTEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENGSLDEMLFSKSCSDTS 419
+ R +D +EELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENGSLD+WLFS+ S TS
Sbjct 121 KIKKDAEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENGSLD+WLFS+ S TS 179

Query 402 NS-RASLTWQORISMAVIVAMGLQWMEHAYPRIVHRDITSSNILLDSNFKAKIANFMA 460
NS +RSTW QRI +A+DVA+GLQWMEH YRIR+HR IT+SNIL+DSNFKAKIANF
Sbjct 180 NSVSSILNRSKLGIMDAVSLQWMEHAYPRIVHRDITSSNILLDSNFKAKIANFLDG 239

Query 461 RTTF 464
+T T
Sbjct 240 KTST 243

>emb|CB12630.3| unnamed protein product [Witis vinifera]
Length=595

Score = 345 bits (884), Expect = 1e-92, Method: Compositional matrix adjust.
Identities = 217/575 (37%), Positives = 320/575 (55%), Gaps = 67/575 (11%)

Query 28 AQQS-QDNNTNTPSPD--SPSCSETVYVYTAQSPNLSUTNISNITDPSPLIARAGNIE 85
+ +Q + + + S L C + Y A SENF L + + +F S L + + N+
Sbjct 27 SQAQPEPNATYPCSNALSSYPCHTFATYATSPNLDASIGDFFVWSRIMISPEGNIS 106

Query 86 FMDKLVKDVLLVPTVTCG-----TGNRSFANISYINQDGSFFVATTSYENLTNMR 140
+ LV Q L VP+ C C T +S+AN+SY I GD+FY V+T S+ NLT + +
Sbjct 87 SPBNPLVAGQSLFVPLNCSCNSVNTTATISYANLSYTIKSGDTFFLVSTFSLNLTYYYS 146

Query 141 VMDNLVPLSNPKLPIGIVQVFFLCKPCPKSNQDREIKYLVITVMKPGDNVSLVSDKFGA 200
V +NS I P L +G +V+P+P+CKCP+ GL + L I +V+P DM+ + V+ G+
Sbjct 147 VEIVNPTLVPTDLDGDKVIFPFCCKPNETQLANGVNLISYVEQSDNLTGVAASLGS 206

Query 201 SPEDIMSENNYQNPATANNLPVLIPVTRLP-----VLARSFSDGRKGGRILPVIIGIS 254
I+ N G N + +PV+RLP V A + R K R VIIG+
Sbjct 207 DTASIIDVN--GDNIQEFT--IFVPSRLPNISQPNVTASVATSVKVE--RKGVIIGLA 261

Query 255 LGCTLLVILVAVLLVYVYCKMKTLNRSASSAETADKLLSGVSGVSKPTMYETDAIMEA 314
+ G L L L+ LK + +N L+ + VS + R +Y + + +A
Sbjct 262 LG--GQDKERPLVGRGTGLKAEV--IMADVBDCLDKYKYGIEELRD 308

Query 315 LTNLSQCKIGESVYKANIECKVLAVKREKEDVTEELKILQKVNHGNNLVKLMGVSSD--ND 373
SE I T SVK I+G+ A+K + K + EELKILQKVNHGNNLV G D
Sbjct 309 TGFSERSLILQSVYKGSIDGELYAIKMKWYAEELKILQKVNHGNNLVLEGGFIDPED 368

Query 374 GNCFFVVEYAENGSLDEMLFSKSCSDTSNRSASLTWQORISMAVIVAMGLQWMEHAYPR 419
C+VYE+ ENGL WL + L W R+ +A+DVA GLQY+HEE PR
Sbjct 369 ATCYLVYEFVINGSLQWLH-----GDRDEKLNWNRIRIADIVAMGLQYIHEHTRF 421

Query 434 IVRKIDSSNILLDSNFKAKIANFSMARTPTNPM-----PKID 472
+R+DI SENLILD N +AKIAN +A+ + + +D
Sbjct 422 VYKIDSSNILLDSNFKAKIANFGLAKSGCNALTMHIVGTQGYIAPEYLDAGGVSTMD 481

Query 473 VVAPGVVLIETLGRKAMTTKNGEVVMIKKDKIFD--QENREKRLKMDMKPR-LES 529
VF+FGVVL+EL+G+G+A+ E G V LW I + E + +R+K RMD L
Sbjct 482 VFSEFGVVLLEISGKAEV--DEGRV--LAMSARGILEGKDEKVKAKRVKVMDEGLLRE 537

Query 530 YYPIDYALSIASLAVNCTADKLSRPTAIVLSL 564
+D + + + +A C T RPA+ +IV +L
Sbjct 538 SCMDNSVINWAVATACTHRDPSKRPBMVDIVYAL 572

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>gb|ABR17803.1| unknown [Picea sitchensis]
Length=536

Score = 343 bits (881), Expect = 3e-92, Method: Compositional matrix adjust.
Identities = 200/516 (38%), Positives = 293/516 (56%), Gaps = 59/516 (11%)

Query 108 NRSPANISYEINQDSGFYPVATTSYENLTNNWRAVMDINPVLSPNKLPIGIGVVPFLCKC 167
      S ANI+Y I G+VF VY++NLT ++V NP L D L IG+V+VF+PCKC
Sbjct 3 NRSGANVPTTYIGQGFYLLSTRKFLNLTYPAVEVNTPTIIVTNLQIGSLATIPCKC 62

Query 168 PSKNQDKELIKYLYTVKPKQDNVSLGDKFKGASPEDIMSENNYGNFTAAANNLVLVILV 227
      PS G+ R LITTV PGD ++S KFGA +++ S N G N T ++L+PV
Sbjct 63 PSNAQVNTQNTKMLITVYVVRPGDTLLNLSQKFGADLQNLRSIN--GINSTLIPYSTLLV 120

Query 228 TRLPVLAR-----SPSDRGKGGIRLPVIGISLOCTLLVILVAVLVV 271
      ++ PVLA-----G+ +IG S+G+ V+ +A+L+V
Sbjct 121 SQKVLQAGPPPPPPPPPPPPVNNATSGGGGLHGAVIGASVGSAAVVCIALLELFCV 180

Query 272 YCLKMKITNNRASS-----EATAKLLSGVSGVSKPTMYETDAIMEAMNMBSE 320
      ++ H+ KL+G+GS V P MY ++ +AR R S
Sbjct 161 VIKRRKSYKQTSISEDQRPPSDVGCKTKSKMLTGISDCVENFMYSLIEDLQATNFBP 240

Query 321 QCKTGESVYKANIEGKVLAVKRKFEDVTEELIKLQVNHGNVLKMGVSDNGDCNCFVY 380
      C I SVYK ++G+ A+K R D++ELKILQVNH NLVL GV ++G +VY
Sbjct 241 LCNIEGVSYKOTLDGHOYAIKLMKGDISQELKILQVNHNLVKGVCISIEGQGSYLY 300

Query 381 EYANGSGLDEWLFSG---KSCSDTNSRASLTWCORISMAVDVAMGLOYMHEHAYPRIVH 436
      EY EN SLA WL ++S S +SL W R+ +A+DVA GLOY+HER P +VH
Sbjct 301 EYENSNLWKLDPESVENMSPTGRSSSLGKQVETRLQVALLVANGLOYHEHPTPVVH 360

Query 437 KDITSSNILLDSNFKAKIANFPMARTTTPM-----PKIDVFA 475
      +DI SSNILLD NF+AKIANF MA+ N PM+-----PK+DVA
Sbjct 361 KDIKSSNILLDGNFRAKIANFGMKAGINALTKHIMTOGYMAPEYLDGVSFSLDVA 420

Query 476 FGVLVIELLTGRKAMTKTEN---GEVVMWKDIKIFDQENREERLKKWMDPKLESY 531
      PRVVI+E++G+A+G+ G+ +LW I + +E+ E +L+K+H+ L+Y
Sbjct 421 FGVLLEIMISGKEALVRENGVPLAGKAGLLTQIFPLEGDE+IEGLKRLWMDNKLQAY 479

Query 532 PIDVALSLASVANTADKSLRPPTAIVLSL 567
      P D ++A+R+ C + +RPP+ EIV LS L
Sbjct 480 TMSDLGVATIRACVEEDPVARPTLEIVYLSNLS 515

>emb|CAN66762.1| hypothetical protein [Vitis vinifera]
Length=591

Score = 338 bits (867), Expect = 1e-90, Method: Compositional matrix adjust.
Identities = 205/567 (36%), Positives = 314/567 (55%), Gaps = 55/567 (9%)

Query 28 AQSQ-QDNRTNFCSPED-SPPSCSTYVYTYAQSFPNLSLTNINISFTDPSLIARASNIE 85
      +Q+G+ N T C+G+ S +C T+ Y A SNFL L +I +F+ S L I+ SN+
Sbjct 27 SQKPEANATQYPCSNLSRSLPCHTFYATSPNLSLALSGLFVWBLIMSPSNI 86

Query 86 FMDKLKVKDQVLLVPTCC-----TNRSPANISYEINQDSGFYPVATTSYENLTNNWRA 140
      + IV O L VY+ C C T S+AN++Y I GDHEY VIT S+ NLT ++
Sbjct 87 SPBNPLVAGQSLFVPLNCSGNSVNATTAISYANLTYIKSGDTFYLVSTFSLNLTYYYS 146

Query 141 VMDELNVLSNPKLPIGIGVVPFLCKCPKSNQDKELIKYLYTVKPKQDNVSLGDKFGA 206
      V +NP L P L +G ++V+P+CKCP++ QL ++L+I+VY++P DN++ V+ G+
Sbjct 147 VEIVNPTLPVTDLDVGKVIPIFCPCPNQTLQNGVNFSLISYVQSDMLGVAASLGS 206

Query 201 SPEDIMSENNYGNFTAAANNLVLVILVITRLPVLAR-----SPSDRGKGGIRLPVIGISL 255
      + N G N C V LV + +V+R+P ++ SP+ + R ITG+R+
Sbjct 207 DTASIIDVN--GDNIPQFT--IFVFSRLNFSIPQNTVATSPATSVRRVERKGAIIIGBI 262

Query 256 G---CTLLVNLVAVLVVYVCL---SMKTL-----NRBASSAETADKLLSGVSGVYS 301
      G C L++L+ VY ++ + K+K + R + L+ +VS +
Sbjct 263 GLVGCGILLVLLIGVWYRHYWVEKIEGDKERLPVGRGSLKAEVNLMADVDSCLD 322

Query 302 KPTMYETDAIMEAMNMBSECKIGESVYKANIEGKVLAVKRKFEDVTEELIKLQVNHGN 361
      R +Y ++A+ SE+ SVYK ++I+G+ A+K+ R + ELKILQVNHGN
Sbjct 323 KYVYGEIELRDTGFPBLSLQSGVSGYSGKSGDELVAIKKMMANYSIELIKLQVNHGN 382

Query 362 IVKLMVSGD--NNGCNQFVUYEYANGSGLDEWLFKSCSDTNSRASLTWCORISMAVDVA 420
      LW+G D D C +VYR+ ENSL WL ++L W R+ +A+DVA
Sbjct 383 LVRLGSPCIDPEDATCYLVYEFVENSLSWLH-----GRDEKLWNRKRLAIDVA 435

Query 421 MGLQYMHAYPRIVHRIDTSSNILLDSNFKAKIANFPMARTTTPMMPKIDVFAFGVVL 480
      GLQY+HEH PR+VH+DI SSNILL N +AKIANF +A++ N +
Sbjct 436 NGLQIHHEHTRPRVYHDKISSNILLDMNRKIANFGLKAGCCN-----AIT 483

Query 481 IELLTGRKAMTKTENGEVVMWKDIKIFP---QENREERLKKWMDPK-LESYYPIDVAL 537
      ++ H+ R V V E+ +R+K RND L +D+
Sbjct 484 MHIVGTQGEKAVDEEGV---LMSARGILEGKDEKVKAKRVKMDDEGLLRSCSMDSVI 541

Query 538 SLASLVANTADKSLRPPTAIVLSL 564
      ++ ++A C T R++ +IV +L
Sbjct 542 NVMAVACTARDPSPRSRSMVDIVYAL 568

>ref|XP_002311653.1| [G] predicted protein [Populus trichocarpa]
gb|EEE89020.1| [G] predicted protein [Populus trichocarpa]
Length=524

GENE ID: 7473444 POPTDRRAFT_564909 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 324 bits (831), Expect = 2e-86, Method: Compositional matrix adjust.
Identities = 188/500 (37%), Positives = 281/500 (56%), Gaps = 56/500 (11%)

Query 110 SPANISYEINQDSGFYPVATTSYENLTNNWRAVMDINPVLSPNKLPIGIGVVPFLCKCPS 169
      S ANI+Y I G+VF VY++NLT ++V NP L D L IG+V+VF+PCKC
Sbjct 13 SSANITYETIAGNTFYIVSTRYQNLITYQVSLNPTLIFELLDYGVEVIFPFCFCH 72

Query 170 NKLQDKELIKYLYTVKPKQDNVSLGDKFGASPEDIMSENNYGNFTAAANNLVLVILV 224
      + Q+ ++ YL+YV++P DN+S V+ FG + I+ N Y P N L P L

```

[illegible]

```
>emb|CA002950.1| LysM-domain containing receptor-like kinase [Medicago truncatula  
var. truncatula]  
length=243
```

Score = 313 bits (80%), Expect = 6e-83, Method: Compositional matrix adjust.
Identities = 158/245 (64%), Positives = 191/245 (77%), Gaps = 3/245 (1%)

[illegible]

```
>gb|EAY87082.1| hypothetical protein OsI_08480 [Oryza sativa Indica Group]
length=651
```

Score = 313 bits (801), Expect = 6e-83, Method: Compositional matrix adjust.
Identities = 205/601 (34%), Positives = 310/601 (51%), Gaps = 85/601 (14%)

[illegible]

```
>ref|XP_001767824.1|  predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ67338.1|  predicted protein [Physcomitrella patens subsp. patens]
length=658
```

GENE ID: 5931014 PHYPADRAFT_132645 | hypothetical protein
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 302 bits (774), Expect = 8e-80, Method: Compositional matrix adjust.
Identities = 211/624 (33%), Positives = 319/624 (51%), Gaps = 84/624 (13%)

[illegible]

```
>dbj|BAI79278.1| LysM type receptor kinase [Lotus japonicus]
length=666
```

Score = 297 bits (761), Expect = 2e-78, Method: Compositional matrix adjust.
Identities = 189/631 (29%), Positives = 327/631 (51%), Gaps = 88/631 (13%)

[illegible]

>ref|XP_002326901.1|  predicted protein [Populus trichocarpa]
gb|EE73651.1|  predicted protein [Populus trichocarpa]
length=609

GENE ID: 7470467 POPTDRAFT_591844 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 292 bits (74%), Expect = 6e-77, Method: Compositional matrix adjust.
Identities = 185/555 (33%), Positives = 301/555 (54%), Gaps = 52/555 (9%)

Query 47	SCETTYTYIAQSNFSLTNTISNIFDTSPLIARASNEPMDRLVKDQVLLVPVTCOT	106
Sbjct 54	SCQAFILFKSG-PFNSVPSISALTSANQELARINNVTRISLSEFTTNNEVI-VFVNCFCF	111
Query 107	GNRSFANISYEINQO-DSFYFVATTSYENLTNWRVMDINPVLSPKPLIGQVFPFLFC	165
Sbjct 112	QYQANVLTQVTTTTSQYVVIANDYVGLSGCAALKHINIHGEYDLPL-GLG++DL C	170
Query 166	KCPKSNQDKKIKYLLTVYVKKPGDNVLSVDKFGASPEDIMSENNYQNFTANNLPVLI	225
Sbjct 171	ACPTNTQMIGTKYLVITYPLSSDDNIPOIDARFKVSTKDI LDANGMEENFTLYPDTTILI	230
Query 226	VFTRLPVLARS-----PS-----DGRKGGIRLPVIGISGCTLLVLVLAVLVVV	271
Sbjct 231	PLPTQTSTSQYTIHNSNFMISPPSALSPPANGSGKKHYSAGLAACSLVLSITAVFVL	290
Query 272	YGLKLN-----KTLNRSASALTA-DKLLSGVSGVSKPTMYETAIMEATNLSQCKIGEV	328
Sbjct 291	SCCKTRKRVSGGRGRKQAVPEDIRVEIASYEQVLKFKFEVVRKATENLSSESRINGV	350
Query 329	YKANIRGKVLAVKRFKEDVTEELKILQKVNHNVLKMGVSSDNGCNFVYYEANGSL	388
Sbjct 351	YAGEFGGEILAVKMGSRDVTKEVNILKRINHLFKLGVC-ENRGCFVLVLEMGESGL	409
Query 369	DEWLFSKSCDTSNRSASLTQWCRISMAVDVAMGLQYMEHAYPRIVHRDITSSNILLDS	448
Sbjct 410	DEWLSCKEETCN-----KAKRIQIALDANGSLYHSITEPAYVHKDKSSNLLNG	463
Query 449	NFKAKIANFSMARFTTNFM-----PKIDVAFGVVLIETLLG	486
Sbjct 464	NLRKAKIANFSIARAATASAKTHVVGSIYMAPEYVRQGTQKTDVYAFGVILLELTG	523
Query 487	RKAMTTKENGSEVVMLEKDIWKIPDGENREERLKKWMDPKLESYPIDYALSLASLAVNC	546
Sbjct 524	KDAVFT-QDGRALLSTEIFSIMEN-RNPEVELDDFFVPAKLGSCGTNFAKILAKVSVAC	581
Query 547	TADKSLSRPTTAEI 561	
Sbjct 582	LMKEPARRPMEEV 596	

>ref|XP_001793589.1|  predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ51621.1|  predicted protein [Physcomitrella patens subsp. patens]
length=637

GENE ID: 5946784 PHYDRAFT_152558 | hypothetical protein
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 291 bits (74%), Expect = 2e-76, Method: Compositional matrix adjust.
Identities = 194/611 (31%), Positives = 312/611 (51%), Gaps = 73/611 (11%)

Query 27	VAQSQQNNTNNSFC-PSDSPPSCETTYTIAQSNFSLTNTISNIFDTSPLIARAS--N	83
Sbjct 1	MAQQNYNDTEGYACNAAPSTSTSCSTFAFYRTQAG-ESLRKVGQYFNKTAAVANVSGNN	59
Query 84	LEPMDDKLKQVLLVPVTCGCTGNRSFANISYEINQDQSFYFVATTSYENLTNWRVMDIN	143
Sbjct 60	LLSTTASLQKQALYVPLDCLNARSQMVSHTVKGTFWLLSVTEYGGTLVYQAMMA	119
Query 144	LNPSFNKLPIGITQVFPFLFCPSKPNQDKKIKYLLTVYVKKPGDNVLSVDKFGASPE	203
Sbjct 120	SNPSKDVYNLGTGDTTIVPFCACPAAQVANGNYLVTTTVYFSETLDIISARFGISPT	179
Query 204	DIMSENNYQNFTANNLPVLPVTRLPVLAR-----SPSDG	240
Sbjct 180	DLRSRNVNSSIIDVNTLLVPLATIPPLATMDWAPVTSQFPSPATVASENAAFAVI	239
Query 241	RKGGIRLPVIGISGCTLLVLVLAVLVVVYCLMKRTNRSASALTADE-----LL	293
Sbjct 240	FKSASQTPYVIGISGAGGLDPLAVFALLILFKASRNSGTFKPLDPEMRKNNVHLELL	293
Query 294	SGSVGVYS--KPTMYETAIMEATNLSQCKIGSEVYKANISGKVLAVKRFKEDVTEEL	351
Sbjct 300	AGMSVMDSGKPVLLSHEELQATQGSFENFIQSGVYKINGQLVAIKQKGNMTQL	359
Query 352	KILQKVNHNVLKMGVSSDNGCNFVYYEANGSLDEWLFSKSC-----SDTSNRSASLT	408
Sbjct 360	KIL+V+H NIVKIL+G+ N++VVEYA++SIL++L+++ S A L	419
Query 409	WCRISMAVDVAMGLQYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARFTTNFM--	466
Sbjct 420	WCSRVIALDVASGLSEYHNTPNPSFVHKDKVKTENILLDNFKAKVAFGMASASADA	479
Query 467	-----MMP-----KIDVAFGVVLIETLLGRKAMTTKENGSEVVMILN	502
Sbjct 480	GPLLTRHITGQGYMAPEYLEHGLTVTRADVAFGVVLIETLSGKEAVVRPEKDEEQQV	539
Query 503	KD-----WKIFQD--KENREERLKKWMDPKLESYPIDYALSLASLAVNCADKSLRS	554
Sbjct 540	KERALSIDIIVNIASTAEALQTEKRPDIQRLSAYPTIASSIASIAMCTDPPDAVR	599
Query 555	PTIAEIVLGLS 565	
Sbjct 600	PSKMDVTFALS 610	

dbj BA179277.1	LM type receptor kinase [Lotus japonicus]
dbj BA179277.1	LM type receptor kinase [Lotus japonicus]
Length=667	
Score = 286 bits (733), Expect = 4e-75, Method: Compositional matrix adjust.	
Identities = 173/591 (29%), Positives = 303/591 (51%), Gaps = 76/591 (12%)	
Query 43	DSPPSSPTVYIAQSNLEINISINIFITPELSIAKRNIMDKRLKQVGLVIVPT 102
Subject 57	DSPPSSPTVYIAQSNLEINISINIFITPELSIAKRNIMDKRLKQVGLVIVPT 102
Query 103	NSVTSQSGYITFKSSRPSEYFISYILNSTPLWAKSNIMTQDTVTITMTVTVE 115
Subject 57	CGCTCGRFANISYEINQ-DSDFVYATGYENILNVAQNDILVFNPKLPIQIQVFP 115
Query 162	PLFCCKPCKNFKDLKYLITLVKVGKGNVSVSKDGSFSDIPDENNYNGQITPAANN 221
Subject 175	PLFCCKPCKNFKDLKYLITLVKVGKGNVSVSKDGSFSDIPDENNYNGQITPAANN 221
Query 222	PLVLIIVTIRLP- - - - -VLARSFSDGRKGIRLPIVIGISGLCTLIVLIVALL 268
Subject 235	PLVLIIVTIRLP- - - - -VLARSFSDGRKGIRLPIVIGISGLCTLIVLIVALL 268
Query 269	VYVYCL- - - - -MKMTLNSSAAETADKILSGVSGYVKFTMPE 307
Subject 374	VYVYCL- - - - -MKMTLNSSAAETADKILSGVSGYVKFTMPE 307
Query 308	TDALMEAFNLSFKSEKNGYSYKIANKEGVKLAVRFEDVTEIKLITVGNKGLKRV 367
Subject 353	TDALMEAFNLSFKSEKNGYSYKIANKEGVKLAVRFEDVTEIKLITVGNKGLKRV 367
Query 368	VSDSDNGCVFYVEYAENSLDLEWFKSSTDSNRASRLTQCRISMAIVAVMGLQYH 428
Subject 428	EYAYIRVHADITSNLTLDNLFKARIANSKARTFTE- - - - - 466
Query 528	NYNIFVLLIKNKLGNVLNGLKFRKAVNSGLPMEKLEMDGDEGGQGTMTRHVQGTGYMP 528
Subject 467	- - - - -MPKIDVAFQVGLLELITGRKMTGARN- - - - -GVEMLLMKITFDQFDE- 514
Subject 529	PETYNENLTPKPDVAFQVGLLELITGRKMTGARN- - - - -GVEMLLMKITFDQFDE- 514
Query 515	REERIKKQVMPKLESYITDYVALSILAVNCTASLAVNCTASLAVNCTASLAVS 515
Subject 515	REERIKKQVMPKLESYITDYVALSILAVNCTASLAVNCTASLAVNCTASLAVS 515
Query 515	REERIKKQVMPKLESYITDYVALSILAVNCTASLAVNCTASLAVNCTASLAVS 515
Subject 515	REERIKKQVMPKLESYITDYVALSILAVNCTASLAVNCTASLAVNCTASLAVS 515

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tbl_xl_XP_002510756.1 [G] kinase, putative [Ricinus communis]
tbl_xl_XF52943.1 [A] kinase, putative [Ricinus communis]
length=634

GENE ID: 6289969 RCOM_1602540 | kinase, putative [Ricinus communis]

Score = 283 bits (724), Expect = 5e-74, Method: Compositional matrix adjust.
Identities = 182/572 (31%), Positives = 289/572 (50%), Gaps = 74/572 (12%)

Query 47 SCCTVYVTAAGSGVNFSLNLSINIF-----DPSLFAIGASVLEMDKRLVKQDVLVFPVC 103
          SC+Y+Y+P + + + TS+ D+ L IA +N+ + + L +V C
          SCQSLVLTFFVYVTPPTVTSVLSFLSGDLSL--IASLNLSD+SVSPFQQQLPFWNC 114

Query 104 CQTNRSPA--NLSYEIQGDSFYT-VATTSYENLRAMVDLNFSPKPLKIGQVVF 161
          C+TNRSPA--NLSYEIQGDSFYT-VATTSYENLRAMVDLNFSPKPLKIGQVVF 161

Query 115 SCFGSGVQFENASITLKFSSFTSYFVANDYTGCLSTQALMSQNFYGDRL--LSVGMRLQ 173
          SCFGSGVQFENASITLKFSSFTSYFVANDYTGCLSTQALMSQNFYGDRL--LSVGMRLQ 173

Query 162 PLRCKPCNKDLKDLKELKYLTVYWKPKVDVSVSKDKGSLDSENNYGNQWFTAAANNL 221
          PL C PC NK DLK DLK ELK YL TVYWKPKVDVSVSKDKGSLDSENNYGNQWFTAAANNL 221

Query 174 PLRCAPCATSGKGLAGFYLLVMTGDTGSLRIGLGVLRVPSGLDANQLSSTISFTPT 238
          PLRCAPCATSGKGLAGFYLLVMTGDTGSLRIGLGVLRVPSGLDANQLSSTISFTPT 238

Query 222 FVLIVPTRLPSVAL-----SPSDRSGRIIRLPVIGLISGLCTPLLIVLAVLL 266
          FVLIVPTRLPSVAL-----SPSDRSGRIIRLPVIGLISGLCTPLLIVLAVLL 266

Query 234 FVLIVLFTPTFTITKASPPFPVSPFPL + P+L SGGSGSKRWTVYVGLGAALLFVNSGF 293
          FVLIVLFTPTFTITKASPPFPVSPFPL + P+L SGGSGSKRWTVYVGLGAALLFVNSGF 293

Query 299 VVVY-----CLNKMTI-----NRASASATADKLKLSGVYSKFTPTDEMAET 315
          +Y + K T+T + SA + + + + + Y + + AT
          LWLFSKSKSKITVTPPSKALQGSBSAVRQSPFMSRSAGVIESITLFIHQDLQAL 353

Query 316 MLYSEKQIGSEVYKXANIGVLAVRKKFEDVTEELIKQVKNWNLKLVMSGSDNNGN 379
          MLYSEKQIGSEVYKXANIGVLAVRKKFEDVTEELIKQVKNWNLKLVMSGSDNNGN 379

Query 342 DYSFENKRIKSGVYSGKPGQDAAVVKRKGDSVSEISLTKIKHNISLRIGVCL--YDAN 412
          DYSFENKRIKSGVYSGKPGQDAAVVKRKGDSVSEISLTKIKHNISLRIGVCL--YDAN 412

Query 376 FCVVYEAENRGLDEWLFPSKSDSNTSRNSKLT--CRQISMAVAMGLCVGLHAEYRIV 435
          +Y+Y+EAENRGL +PSKSDSNTSRNSKLT--CRQISMAVAMGLCVGLHAEYRIV 435

Query 413 TPLYVEFAENRGLAE-----NVQTLKQGVQIAHVADALNLTINPTNPEYI 460
          TPLYVEFAENRGLAE-----NVQTLKQGVQIAHVADALNLTINPTNPEYI 460



Query 461 HRDITSSNLLDMSFKRAITAFMSKATFTNP--NM 468
          + + + + SNILLD+ AKTANP +ART +
          HMKLTSNLLDMSFKRAITAFMSKATFTNP--NM 468

Query 469 PKIVDFAGFVYVLIETLTKAGKATFKENGVEVWMLKMDIKWIPQGENRRELRKKMDPKLE 520
          PKIVDFAGFVYVLIETLTKAGKATFKENGVEVWMLKMDIKWIPQGENRRELRKKMDPKLE 520


Query 521 KLVDFVAFVGLLLELSSKATYVNRAREMSKIRV--LSDNVHRLGLMDPPLSG 579
          KLVDFVAFVGLLLELSSKATYVNRAREMSKIRV--LSDNVHRLGLMDPPLSG 579

Query 529 SYPTDVALASLALANVCADKSLRPTAEI 560
          +P+D A BJA IA C +R+
          KQPLDVALASLALQALQCTISDINDAREFSQV 611

```

>ref|XP_002522569.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor,
putative [Ricinus communis]
gb|EF39869.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor,
putative [Ricinus communis]
Length=624

[illegible]

```
>ref|XP_002990805.1|  hypothetical protein SELMODRAFT_l1326 [Selaginella moellendorffii]
gb|EFJ08078.1|  hypothetical protein SELMODRAFT_l1326 [Selaginella moellendorffii]
length=539
```

Score = 280 bits (717), Expect = 3e-73, Method: Compositional matrix adjust.
Identities = 190/552 (34%), Positives = 295/552 (53%), Gaps = 31/552 (5%)

Query	38	FCSPPDSGCTCTYTAIAQSPNFSLISNINIFDTPSLIRARASIMEDMKDIUKQVL	97
Subject	1	+SC S+SC S+ Y +A +L +L +E +S +A +S +A +S +L V DV	100
		YSCVSNST-SGCAATFANIASQDQD-TLQSVGLRATFVSEQLAEASQI-AQSATLPPQVQL	
Query	98	LVITVTCGTGNTAFANISQDQDQYFVATTSVETLITWRAWMDVFLVSNKELQI	156
Subject	57	LVITVTCGTGNTAFANISQDQDQYFVATTSVETLITWRAWMDVFLVSNKELQI	157
		LIPLNCSGACSGKQFNATYIIGSTGLIVLSNGTGTGLITTVQAEANPLVPTLQGD	116
Query	156	QVFLPCCGKCPMKQLDKELKYLITVTKVQGDVLSVKDFSGAESIDEMSNYQNFPA	217
Subject	117	+VEP+ C CPS Q+ L +LT+ P+ Q+ + + + S +S +N + +T	176
		SIVTFIRACAPCSAAQVAGVSLTIVSIWFGELDGIACANMVSRGLASLDNVSGSATL	176
Query	218	AKNLPVLVLTPLVLARSPDSGKRGIRLPIVIGISGCTGLVLVLVLVLYVYCLMK	237
Subject	177	+ + + + + S + + + + +G+I+ + C VL+ +V +L +V +L	237
		SPAPFPPANNFPMNSPFDPSGSSSSSGNFG+YGVIAVCVAVLVLVVALVPIRRSR	244
Query	278	TLNRSSASGATADK- - - - -LLSGSGVQ- - -SKPMFYETAIMEATNLSQKIQIS	328
Subject	235	LI+G+ S+ P+ + + + +T N+ S+ T+ V	328
		YK+KASVYAPSPKQSPHPHALLAMGHLVDREPRFVVSYLEBDCDNTNFSASHLQGV	294
Query	329	YKANTEKVLKVALEPKEDVT-ELAKILQVHNVNKLKLVHNSGKCPVVEYAEKNS	384
Subject	295	Y+ + + + +A+ K +T +ELKIL KV+H NKLK+ S+ D +P+VEY+ADNS	384
		YRGLIKLVAIKEMKGGTTSQELKILKVHNSHNSGKICGSD-KLFIPLVADNGS	353
Query	388	LDWLKFLSCDTSNLSGNTLQCRISMAVDVAGLYQYHEAVPIRVHIDTSSNTLL	407
Subject	354	- - -SC A+ M +D+VA GL+QGL+ + +VH+D+SSNTLL	407
		LDWLKFLSCDTSNLSGNTLQCRISMAVDVAGLYQYHEAVPIRVHIDTSSNTLL	407
Query	408	SNFRKATKSNMPTATMTNP- -MMPKIDVAFGVILLTQKMTKNTKMGVVMKAKDI	505
Subject	408	SNFRKATKSNMPTATMTNP- -MMPKIDVAFGVILLTQKMTKNTKMGVVMKAKDI	505
		SNFRKATKSNMPTATMTNP- -MMPKIDVAFGVILLTQKMTKNTKMGVVMKAKDI	505
Query	506	N- - -KIQEENRE- -ERLKKMMQPKLSEYPIYDIALSLAVNCKTSGEPIRATPE	559
Subject	466	+ + + + +E +L+K W DP L+ P D AL+ +A +C + +RP+ + +	559
		FVKLTGTFAGCDNTEKLEKHADPILNCAVADILNFEVARSVCVADPDPMMKD	527
Query	600	IVLSLSLTLS	539
Subject	528	IVLSLSLTLS	539
		IVLSLSLTLS	539

>ref|XP_002277331.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length=638

GENE ID: 100258108 LOC100258108 | hypothetical protein LOC100258108
[Vitis vinifera]
Score = 280 bits (716). Expect = 4e-73. Method: Compositional matrix adjust.

Identities = 188/628 (29%), Positives = 313/628 (49%), Gaps = 94/628 (14%)

Query 17 LVIMLESTNVAQSQD-----NRTN-FSCSPSPSCCTEYVYIAQSNFL 62
 Sbjct 1 MVLLLVMIWVAQAQSSVNNHGLDCNNFNENFTGPGC--NGRSCSHYLTFRSAPPDY 58

Query 63 SLTNISNIFDTSPLSIRASNLPEMDKLVKQDVLVPTVCGCTGNRSFANISYEINGQD 122
 Sbjct 59 SPPIAYLINESPAQIATINEVSDVD-TSKDITVLVIVNVCSSGDFYQHNFTYTKASAS 117

Query 123 SFYE-VANNYSYENLNMRAVDLNVLSAPNKLPIGIVQVPELCKPCKSNOLDKIKYLI 181
 Sbjct 118 ETYESLATTYVLTGAVQWALQVDFYDNR-LVSGHQLQVFMCACTANQAGFNLYL 176

Query 182 TVYWKGDNVSLVSDKFGASP-EDIMSENNYQNFATAANNLPVLPVTRVPLARS---- 236
 Sbjct 177 SYVTWGDITDSIAKIFGVDVQGSFYDANRLSTSVIYPTFTLVPLKNPFSKIQTVTS 236

Query 237 -----PSDGRKGIRLPIVIGISLGLTLLVILVAVLVVYVCLMKY----- 278
 Sbjct 237 PPAPSPETPMVPSGGSSSSKAWFVIGAGIGALLVLLISSGMMFCFRRRQSGQDKIV 296

Query 279 -----LNRASASATADKLKSGVSGVSKPTMYETAIMEATMNLSECKIKGESVIK 330
 Sbjct 297 LDIQEATKLKSLNKTMSISLEGIRIEMESLTVYKEELQAAGYFGEANRIGKSVR 356

Query 331 AMTEKGLVAVKRKEDVTEELKILQVNHGNLVKMGVSSDNDGNCFFVVEYAENGSLDE 390
 Sbjct 357 ASFGKDDAAIKMMKQDVSEELILQINHSKIVRLSGPCI-HAGNTYLVVEYAENGALRD 415

Query 391 WLFS--KSCSDTSNRASRLTWQRI SMAVDVAMGLQYMEHAYPRIVHRDITSSNILLDS 448
 Sbjct 416 WLHSGDGLTCS-----TLGKGRVQLVADADALYINLNTISFPCIRKMLKSNILLDG 468

Query 449 NPKAKIANFSMARTFNE-----MMPKIDVFAFGVVL 479
 Sbjct 469 NMGKGVNIFGLARLNEGDEGGGLQITRHVVQYQYMAPEYVENCVVTFKLIDFAFGV 528

Query 480 LIELTLGRKAMTT--KENGESVVLAKDKIKWIFDGENREERLEKWMKPLESYYPIDYAL 537
 Sbjct 529 LIELTLGKEAAPSQKKEGEGELSV--SINEVL-QSDNVRDKLGFIDPCLAHEYFPDLAF 585

Query 538 SLASLAVNCTADKLSRPTIAELVISLS 565
 Sbjct 586 SMAQLAKSCVADHLNARPTMSDIPVILS 613

>ref|XP_002974494.1| [G] hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
 gb|EF24716.1| [G] hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
 Length=539

GENE ID: 9657733 SELMODRAFT_11327 | hypothetical protein
 [Selaginella moellendorffii]

Score = 279 bits (714), Expect = 7e-73, Method: Compositional matrix adjust.
 Identities = 189/552 (34%), Positives = 294/552 (53%), Gaps = 31/552 (5%)

Query 38 FSCSPSPSCCTEYVYIAQSNFLTNISNIFDTSPLSIRASNLPEMDKLVKQDVL 97
 Sbjct 1 YSCVSNST-SCQAYAYRALQGD--TLQSVGLRFLRSLVEQLASQI-AQSATLVDPQVL 56

Query 98 LVPTVCGCTGNRSFANISYEINGQDYSFVATTYSYENLNMRAVDLNVLSAPNKLPIG 157
 Sbjct 57 LIPKNCASGSGSPNATYIQSGDPTLVNNGTFFGLTQYQVARNAPLAVPTMLQGD 116

Query 158 QVPELCKPCKSNOLDKIKYLIIVYWKGDNVSLVSDKFGASPEDIMSENNYQNFATA 217
 Sbjct 117 SIPEPIRCAPSSAAVAGVSTLVTSYIMPGEILLDGIARAANNVSRTRLASDNTVSGSALT 276

Query 218 ANNLVPLVLPVTRVPLARSNSDGRKGIRLPIVIGISLGLTLLVILVAVLVVYVCLMK 177
 Sbjct 177 SPAAPPANPPNPNSSPSSSSSSSGSTGM--YVGLIACVAAVLVLLVILVIFIRRRR 234

Query 278 LNRASASATADK-----LISGVSQGV--SKPTMYETAIMEATMNLSECKIKGESV 328
 Sbjct 235 KVTASASYAEPSKQPSHAPLHAGMLGVDSEKPVFVSYEELCDATNFSASHLIQGSV 294

Query 329 YKANIEKGLVAVKRKEDVTEELKILQVNHGNLVKMGVSSDNDGNCFFVVEYAENGSL 387
 Sbjct 295 YAGILRKLQVAKIMKGGTTSQELKILCVHSSNLVGLIGISGDD-KLFLVVEYADNGS 353

Query 388 LDEWLFSKSDTSNRASRLTWQRI SMAVDVAMGLQYMEHAYPRIVHRDITSSNILLDS 447
 Sbjct 354 -----SSGTLNPTATATLQVMDVATGLYTHVYTRFSFVHWRSSNILLD 407

Query 448 SNFKAKIANFSMARTFNE--MMPKIDVFAFGVVLIELTLGRKAMTTKENGESVVLAKDK 505
 Sbjct 408 ANLRKAVNFMARLVLTHGFTPTKDVVIAFGVVLLEFTGREALISTSGSEKQYLADA 467

Query 506 W----KIFDQENRE--ERLKKWMKPLESYYPIDYALSASLAVNCTADKLSRPTIAE 559
 Sbjct 468 FVKLTGDFAGSDNDKEIKLHMADPILONAVPMIDALNFVEVARS CVADPFDARPNTRD 527

Query 560 IVLSILTLTPQS 571
 Sbjct 528 VTFKLKSLSS 539

>emb|CB117583.3| unnamed protein product [Vitis vinifera]
 Length=1305

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position
 Score = 277 bits (703), Expect = 3e-72, Method: Compositional matrix adjust.
 Identities = 171/565 (30%), Positives = 298/565 (52%), Gaps = 56/565 (9%)

[illegible]

Score = 273 bits (698), Expect = 6e-71, Method: Compositional matrix adjust.
Identities = 177/557 (31%), Positives = 297/557 (53%), Gaps = 56/557 (10%)

[illegible]

```
>ref|XP_002510333.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
```

gb|EEF52520.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
Length=637

GENE ID: 8260932 RCOM 1593420 | serine-threonine protein kinase, plant-type,
putative [Ricinus communis]

Score = 276 bits (707), Expect = 5e-72, Method: Compositional matrix adjust.
Identities = 169/555 (30%), Positives = 295/555 (53%), Gaps = 49/555 (8%)

[illegible]

```

Sbjct 171 CP++Q+ E KYL+T+ D+++ ++F S E I+ N ++T + +LIP
CPTASQVRNTEKYLLTPFISDHIAAERFNVSKESIIDANGLESPTIYPDTTILIP 230

Query 227 VTRLVPLAR-----SPSGRKGIRLPIVIGISLCTLLVLVLVLVV 271
+T P ++ SP D R+ +L +G1+ C+LVL +V++++
Sbjct 231 LTPESQSTIIHENPTEVSPPLASPPDNRKRKLYEKVGITACSLVLVLSIIVLIFL 290

Query 272 YCLMKTLNRSASSAETA DKL LSGVSGVSKPTMYETDAIMFATMNLSECKIGESVYKA 331
+++++ + + +AT N S + I SVY
Sbjct 291 LAKDRHKFFPRINRRREQDRLRLIASVSGILKVFGLSEVKKATIDFSSKHIIKSLIYWG 350

Query 332 NIEQRLAVKAFKEDVTEILKIQKNVHNLVKIMVSSNDGNCFTVYVEAENGSLDQW 391
G++L+K+ DV++E II++NR NIKL GV +N G ++ +Y +NGSE LW
Sbjct 351 EFNQQLIALKMNNDVSKVNI LKRNHFNILKILGQW-ENLCOPYLFFYYMKNQSLQW 409

Query 392 LFSKSCSDTSNRSASLTWCQRIAMAVDAMGLQMYHEHAYPRIVHRDITSSNILLDSNFK 451
L + D +W QRI +A+D+A GL Y+H P VH+DITS +ILLD+N +
Sbjct 410 LSGRETFDVG-----SWNRIQIALDIANGLYLHSPTEFACVHKDITSGHILLDNLA 463

Query 452 AKIANFSMARTTNNM-----PKIDVFAFGVLELLTGK 489
KIANFSA A PKIDVFAFGVLELLTGK
Sbjct 464 AKIANFSAARAANAVALIKRTEGTROYMAPEYVQAQGVTPKIDVFAFGVLELLTGKDA 523

Query 490 MTKNGEVMWKKDIKIFLQDEENREERLKKMDPKLSEYYPIDYALSLASLAVNCTAD 549
+ ++ G+ +L K I+ ++ EN E L +DP AL LA +++ C
Sbjct 524 VFMKD-GKETLLSKAIFVSMVK-EMAEAE LAFVDPSPFTGGQSKLALRLARVSLACLTQ 581

Query 550 KSLSRPTIAEVLISL 564
RP++ E+V +L
Sbjct 582 VPARAKSMGEVSTL 596

```

>dbj|BAI79276.1| LysM type receptor kinase [Lotus japonicus]
Length=633

Score = 276 bits (70%), Expect = 7e-72, Method: Compositional matrix adjust.
Identities = 193/612 (31%), Positives = 315/612 (51%), Gaps = 93/612 (15%)

```

Query 38 FSPCSDSP-PSCEITYVTYIAQSPNLSLTNINIFTDPSLISARASNLPMDDKLKVDQ 96
++C S ++C+ Y+T+ Q P + S+ IS + + +A ++ + +
Sbjct 49 YTCNGSANHTQAYLTFRTQ-PYNSVYITISLTSADARHLAETMSVS-QNTTFETNKL 106

Query 97 LVPVFCGCTGNRSFANI+SYEINQGSDFYVATTSYENLTNWRAMVDNLVLSPNKLEPG 156
+VRY C C G AN SV +D+ + + +E IT +A+M N +P L +G
Sbjct 107 VLVFQVCSCAGEYQANTSYAFQNTDTPESIANNTFGLTQCALMHENH-NFGHLYIG 164

Query 157 IQVVPFLCKCPKRNQDKIKYLLTVVKKPGDNLVLSVDFKQASPEDIMSENNYQGNFT 216
++ PL C CP+KNQ +K IKYL++Y+ GD++S++S+KFG S + + N+ + T
Sbjct 165 RELTVPLACAPCTKNQTEKIKYLLSVLVNMGDSISVISEKFGVSCNNTLEANS--SLT 222

Query 217 AANNL-----VLIPVTRLVPLARS-----PSDGRKGIRLPLVIGISL 256
A P +L+P+ + + + L V++G C
Sbjct 223 KAKIYPFTLLVPLHDKFNSNQTIIQSPSTSSPPSSSTHQSNNKTKLVYVVG--G 279

Query 257 CTLVLVLVLVLVLVVV-----CLMKTLNRSASSAETA DKL LSG-----VSGVYS 301
++ ++ +V+ L T+ S + + + G
Sbjct 280 VFALVLTAVIPFCHYHKGRKKDDLSQLTVSSEFENQQLGKMKMGDKGLSEFTHGIA 339

Query 302 KPMTEYTDAMFATMNLSECKIGESVYKANIEGKVLAVKRFEDVTEELIKLVKNVHN 361
+Y + I AT N L+ I SVY+ + G +A+K+ + DV++E++L KVN N
Sbjct 340 SEKVSFEETQATNLMSSSLKSGSVYGVNMGDLVAIKTEIGDVSKEIQLIKVKNHNS 399

Query 362 LVLMGVSSNDGNCFTVYVEAENGSLDEMLTSCSCSDTSNRSASLTWCQRIAMAVDAM 421
++E GVS N+Q ++VETEA NQ L EM+P L+M QRI +A+DVA+
Sbjct 400 VIRLSGVSP-NEGQWLYLVEYAANGPSEIMFFCKF-----LSWTQRIQIALDVAI 449

Query 422 GLQVMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTTNN----- 466
GL YH P +R+D SNNILDS+F+AKIAN S+AR+
Sbjct 450 GLDYLSHSTSPPHIKDKLSSNNILDSDFRAKIANLSLARSVKGVEDDDQFLATRNIVGT 509

Query 467 ---MMP-----KIDVFAFGVLELLTGK--AMTKEGEVVMKMDIKFIDQ 511
M +K+DV+AGV++E+ITG+ A+ ++N K+
Sbjct 510 RQYMAFVYENGVLSTKIDVFAFGVLELLTGKREVAIILADNN-----NLSGVLSEA 563

Query 512 EENREERLKKWGVSGVYPIDYALSLASLAVNCTADKSLSRPTIAEVLISLALLTPB 571
EERLK+MNDP +S YP +A+ + V C +SHP+ EIV L S T S
Sbjct 564 VLG-EERLKEKMDPSIQNYPFELAMFVEIIVGICEKDPASRPMQEIPTLS-RTMNS 621

Query 572 PATLERSLTSSG 583
+ E S+ SC
Sbjct 622 SLWSEMSVNIIG 633

```

>dbj|BAI79286.1| LysM type receptor kinase [Lotus japonicus]
Length=633

Score = 276 bits (70%), Expect = 8e-72, Method: Compositional matrix adjust.
Identities = 192/612 (31%), Positives = 315/612 (51%), Gaps = 93/612 (15%)

```

Query 38 FSPCSDSP-PSCEITYVTYIAQSPNLSLTNINIFTDPSLISARASNLPMDDKLKVDQ 96
++C S ++C+ Y+T+ Q P + S+ IS + + +A ++ + +
Sbjct 49 YTCNGSANHTQAYLTFRTQ-PYNSVYITISLTSADARHLAETMSVS-QNTTFETNKL 106

Query 97 LVPVFCGCTGNRSFANI+SYEINQGSDFYVATTSYENLTNWRAMVDNLVLSPNKLEPG 156
+VRY C C G AN SV +D+ + + +E IT +A+M N +P L +G
Sbjct 107 VLVFQVCSCAGEYQANTSYAFQNTDTPESIANNTFGLTQCALMHENH-NFGHLYIG 164

Query 157 IQVVPFLCKCPKRNQDKIKYLLTVVKKPGDNLVLSVDFKQASPEDIMSENNYQGNFT 216
++ PL C CP+KNQ +K IKYL++Y+ GD++S++S+KFG S + + N+ + T
Sbjct 165 RELTVPLACAPCTKNQTEKIKYLLSVLVNMGDSISVISEKFGVSCNNTLEANS--SLT 222

Query 217 AANNL-----VLIPVTRLVPLARS-----PSDGRKGIRLPLVIGISL 256
A P +L+P+ + + + L V++G C
Sbjct 223 KAKIYPFTLLVPLHDKFNSNQTIIQSPSTSSPPSSSTHQSNNKTKLVYVVG--G 279

Query 257 CTLVLVLVLVLVLVVV-----CLMKTLNRSASSAETA DKL LSG-----VSGVYS 301
++ ++ +V+ L T+ S + + + G
Sbjct 280 VFALVLTAVIPFCHYHKGRKKDDLSQLTVSSEFENQQLGKMKMGDKGLSEFTHGIA 339

```

```

Query 302 KPTMYRTDAIMEATMNLSEQCKIGRGSVYKANIEGVIAVAKRFKEDVTEELKILQKVNHN 361
          + + + + + I AT NLA P I SVY+ + G +A+K+ + DV+H+I+L KVNH N
Sbjct 340 SFKVPYSEYIGBATNWINSSSLIKGSVYGVWNGDGLVAKTEKGGDSVSEIQLKVNHN 399

Query 362 LVKLMSVSDNDNCVFPVYEAENGSIQDLWFSKSCSDTSSNRASLTMCQRTSMVAOVAM 421
          ++I GVS NG+ +VEXA NG I EW+P L+W QR+ +A+VAI+
Sbjct 400 VIRLSGVSP-NEGQWLVLYEYAANGPSEWIFGFK-----LSWTRQRIQIALDVAI 449

Query 422 GLQYMHEHAYPRIVRHDTISNNILLSDNFKAIANFSMARTFTNP----- 466
          GL Y+H P +H+D SNNILLDS+FKIAN S+AR+
Sbjct 450 GLDYLSHTSPPHIKDLKSSNILLSDNFKAIANSLARSVKGVEDDQFLATNIVGT 509

Query 467 ---MMP-----KIDVFAEGVWVLIETLLGRK--AMTTEKNGGEVVMKMDIKFIQD 511
          M P + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 510 RGVYMAPEYVLENGLVSTKLIDVYAGVLMLEITRGKVAAILAEDNN-----KNLSGVLSA 563

Query 512 EENKEERLAKKMDPKLESYYPIDYALSLASIAVNCTADKSLRPETAEIVLSLSLTQPS 571
          EERLK+MDP L+S YP + A+ + + V C SRP+ EIV +S T S
Sbjct 564 VLG-EERLKEMDPSIQSNYPFELAMVFVEIIVGCIKEDPASRPMQIVPTLS-RTMNS 621

Query 572 PATLERSLTSSG 583
          + E S+ SG
Sbjct 622 SLRSGMSVNISSG 633

```

```

>gb|AB059612.1| LYK4 [Glycine max]
Length=633

Score = 270 bits (68%), Expect = 5e-70, Method: Compositional matrix adjust.
Identities = 191/646 (29%), Positives = 329/646 (50%), Gaps = 90/646 (13%)

```

```

Query 4 FFPFLPHSLQCLVLMISTNIVASQSDNRTNFSCP-----SDSPSPSCT 50
          PEP+P+ I L+I FS I+ Q +CP + + SC+
Sbjct 3 LEFFPII--IIFTLIRNFSGL-QGQPIYGITGACPRRCKNNISRGTYCNGANHSQC 59

Query 51 VVYVYIAGSFNFIISLTINISNIPDSPLIARAGNLEPMDDKLVKDQVILVPTGCTGNRS 110
          Y+H+ +S S+ IS + + + P+AT + + + + + + + + + + + + + + + + +
Sbjct 60 YLTFRSQ-PITYNSKISTILGSDPSGLAKINSVS-MNDTETNKLIVFPVNCSCAGEY 117

Query 111 FANISYEINQGSDFYVATTSYENILNMAWMDLNPVLSPNKIPIGIQVFPFLCKCPK 170
          N SYE + + + + + A +E LT +A+ + N -P + G + + + PL C CP+K
Sbjct 118 QZNTSYEFHNSBTETLIANNTPFEGLTTQALEGNH--NPANIPGRRLLVFLRCACPTK 175

Query 171 NQLDKETKYLITVWPKGDVNSLVSKDGASPEDIMSENNYGNQFTAAANLP---VLIPV 227
          NQ + K I+V+Y+Y GD+V+ S+XG + + N P A P +L+P
Sbjct 176 NQTEGRVILVSLVWMDGSVSEKPGQVNMFTLEANTL--TLQCATVYFTTILVFL 233

Query 228 TRLVPLARSPPDGGKGGIRLVITIGISLGCTLL-----VLVLAVLLVYVYCLRMK 277
          P + + S S+ T + + + + + + + + + + + + + + + + +
Sbjct 234 HDKPSSSQTVSPRTKTPPPSPSSDSSSNKTWVYVGVVGAIALSVLCVAFIFTRYR 293

Query 278 TLNRASSA-----ETADKLLSGVSGYVKPTMYETDAIMEATMNLSEQ 321
          + S + + + + + + + + + + + + + + + + +
Sbjct 294 KNRKKGDSVVGSKSFAIEEKPEKVNKELSIIGIAQSFVYNFELQKATDNFSP 353

Query 322 CKIGESVYKANTSGKVLAVKRFKEDVTEELKILQKVNHNVLKMGVSSDNDGNCVFPV 381
          + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 354 SWIKGSYGVINGDGLAATRIEGDSKSEIEIIMKINHSNIVLSGVSP-HEGSMVLYVE 412

Query 382 YAENGSLDEWLFKSCSDTSSNRASLTMCQRTSMVAOVAMGLQYMHEHAYPAIVRHDTIS 441
          YA NG L EW+ + + + L+W QR+ +A+DVA GL Y+H P +H+I S
Sbjct 413 YAAAGDLSIEWIYFHNVG-----KFLSWTRQRIQIALDVATGLDYLSHTSPPHIKDINS 467

Query 442 SNNILLSDNFKAIANFSMARTFTNP-----KIDVFA 475
          SNNILL +P+ K+ N S+AR M P
Sbjct 468 SNNILLDGDGRVNTLSLAKCLEGGDDQLPATRHIVGTGVMAPYVLENGLVSTKLIDVYA 527

Query 476 FGVLVLIETLLGRK--AMTTEKNGGEVVMKMDIKFIQDEENKEERLAKKMDPKLESYYP 533
          FGVA + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 528 FGVLVLEMTVGEKVAAILTEDZKLSHVLISGLG---EESGEMKLEFVDFSLGENCPL 583

Query 534 DYALSLASIAVNCTADKSLRPETAEIVLSLSLTQPSPATLERSL 579
          + A+ + + NC SRP+ EIV S+S T S + ERS+
Sbjct 584 ELAMPVTEIMDNCIKTDPASRPSVHEIVQSMBS-RTLASLSLWERSM 628

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```

>emb|CB10796.3| unnamed protein product [Vitis vinifera]
Length=680

```

```

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position
Compositional matrix adjust.

Score = 269 bits (68%), Expect = 1e-69, Method: Compositional matrix adjust.
Identities = 170/518 (32%), Positives = 279/518 (53%), Gaps = 45/518 (8%)

Query 70 IFDTSPLSIARASNLPEMDKLVKDQVILVFPVTCGCTGNRSFANISYEINQGSDFE-VA 128
          + + + + + IA + + + + + K+ KD VL+VPV C +G+ N SY + + YF +A
Sbjct 151 LKNSNPDIATINIGSDVN-KIKPDTVLIVFPVNCSCGHFYQNASYFLAYDFENYTLIA 209

Query 129 TTSYENTLNMAWMDLNPVLSPNKIPIGIQVFPFLCKCPKSNKLDKEIKILYITVWKP 188
          +Y+ T+ S+ + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 210 NNTYQGLTQJCKAHNPNYYRN-LSVGGDLLVPMICAPTANQTAAGFNLYLTIVTWKG 268

Query 189 DMVSLVSKDGASPEDIMSENNYGNQFTAAANLP-----PVLIPVTRLEVLARSP-- 237
          D +S +D PG +DI Q+ AN+L P+L+P+ P + +
Sbjct 269 DYISSIADTFGV--DDI-----QSIFDANSLSDDLIFPFTLVLKRNPPTRIQTTLIS 319

Query 238 -----SDGKGGIRLVITIGISLGCTLLVILVYVYCLRMKTLNRASSA 287
          + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 320 PPPPSVPVPPGGGASDKMWYVGVIGATLVILMPSGII--CTKKPSYMSGENNISL 387

Query 288 TADKLLSGVSGYVKPTMYETDAIMEATMNLSEQCKIGRGSVYKANIEGVIAVAKRFKEDV 347
          + G+ V T+Y+ + +A E + I Y+ I+G A+K K DV
Sbjct 378 SVSS--GGIHUAVESLTYYEYKELQAAGPFGEANRIGCVYRGLIGDDAAIKMKMGDV 435

Query 348 TEELKILQKVNHNVLKMGVSSDNDGNCVFPVYEAENGSLDEWLFKSCSDTSSNRASL 407

```

[illegible]

>ref|XP_002269442.1| PREDICTED: hypothetical protein [Vitis vinifera]
length=632

GENE ID: 100264999 LOC100264999 | hypothetical protein LOC100264999
[Vitis vinifera]

Score = 268 bits (685), Expect = 1e-69, Method: Compositional matrix adjust.
Identities = 170/583 (29%), Positives = 296/583 (50%), Gaps = 69/583 (11%)

[illegible]

```
>ref|XP_002533279.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
```

```
gb|EF29111.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
length=617
```

GENE ID: 8272991 RCOM 0411670 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 265 bits (676), Expect = 2e-68, Method: Compositional matrix adjust.
Identities = 187/601 (31%), Positives = 315/601 (52%), Gaps = 78/601 (12%)

Query	22	FSNIVIAQSQQDNRTK	---TSCPSDPPSPCKCT	YQSGNFI	LSLNI	IFDFTB	77
Sbjct	25	SV NIV + + T + S +	SCIT+Y + Q + P + + + + I S +	+	+	+	83
Query	22	FSNIVIAQSQQDNRTK	---TSCPSDPPSPCKCT	YQSGNFI	LSLNI	IFDFTB	77
Sbjct	25	SV NIV + + T + S +	SCIT+Y + Q + P + + + + I S +	+	+	+	83
Query	27	TARASNLEENDKQVLQVLPVTC	CGNRSAFN	YIIN	-NGQDS	YVATTS	36
Sbjct	84	IA + N + L + + + V P + C C +	AN SY I + D + + + A + Y E L +				
Query	137	NLRAMVNI	LPVLSNKLIGIVQVPP	FLCKPSK	NRGLIK	XYLYTKWR	142
Sbjct	143	TCSNLSMQNN	-YSFSDSDGKRLVPLRCACPT	NSQSGNAT	XYLYTSVSDGKRVASE		201
Query	143	KFGASGDSIESNNYQGMPTANL	YIVLP	ITVRL	PL	-LARS	242
Sbjct	202	YF AS + + N Y ST	L P T + + L + PS				
Query	202	YF AS + + N Y ST	L P T + + L + PS				
Sbjct	202	YF AS + + N Y ST	L P T + + L + PS				
Query	243	CGTCL	-LPVLSNKLIGIVQVPP	FLCKPSK	NRGLIK	XYLYTKWR	142


[illegible]

```
>ref|XP_002533278.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor,
putative [Ricinus communis]
gb|EEF29110.1| BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor,
putative [Ricinus communis]
length=647
```

GENE ID: 8272990 RCOM_0411660 | BRASSINOSTEROID INSENSITIVE 1-associated
receptor kinase 1 precursor, putative [Ricinus communis]

Score = 265 bits (676), Expect = 2e-68, Method: Compositional matrix adjust.
Identities = 181/601 (30%), Positives = 306/601 (50%), Gaps = 87/601 (14%)

Query	3	DWRTFSDDSDSPSCCTVYVYTAQSPFLSNLTINISFTPLSTRANLSEIMDDKVL	92
Subject	42	+ + +3C + + SC +CT+Y+T + + C + + + + + I S + + + P + + N + N DSALGYSC -NGLNTSNCFQNFVIFSRSPQ -TVNTVTSISBQSLM+QSVSATEFTD	98
Query	43	KDQVLVGLQKQCGNRSAFNLINQSGDSYFVATSYENLTNMRQMLNVPFSLNK	152
Subject	99	TNKLIVFVPMNCCSGSDYQFVITVQVQADAPFANNTVQLSTSCQALONQNRQTVD	158
Query	153	LPIGIQVFLPFLCKPSKQDLKEIKLYITVFKNGQVSLSDFKGASPDIMENBYN	216
Subject	159	P I + + L I + PLAC C+KND D IKYL+V + GD VS VS KFG + + N FPNEL -LRI PLAC CPTKNTDAGIKLYITVLTVDVSAV+FGKGTNGSLAENGSL	217
Query	211	-QNF+ANNPLVILPENTRALV -	272
Subject	218	EQTPTVFPETLLIPLENPTNSQTIISPPFPPASSPPPPSTDPNGSSKAGKWWYVL	277
Query	253	ISLGTQILVLVLVLLVLYVL -	293
Subject	278	+ G + V L I + + + Y L + + K+L+N + E + L VLAG -+TVLGLVILYIYALFRSRKRKEPIIVSESTFAKSGKLNKL -EQESQD	298
Query	294	SGVSGYVSKPVTDEIATAENNLSSCKQESVYCANIEGKVLKAFKVDPEIKEL	353
Subject	341	SSIAQAQIKVYVGLKFEALANTSCCMKIGKSGVGYQISDVA+KLVNGVGLPEIK	392
Query	394	IQKNVNLVYVSSSDNDCTNVVYVAENSGSLDMLSKSCSDSNSASLTCRAI	413
Subject	393	KVXN NLV+ + V + G + + +HYVZA NGAL -W + + + - - -SNEGNFLSWTOR	416
Query	414	BNADVGVQYMEHAYPRATVIRH+DITSSNLFDSNFKANFMASTFTNFP -	466
Subject	447	+A+DVA GL Y+R P +HDI SGN+LDS+FKANFAN +MAR+ QIALDVAIGLVNLYHSTSPPHHIKKNSVLDSDPFKANLMAJSTGEQDEFAIT	466
Query	467	-MM- -	505
Subject	507	RIHVTQGYMAPEYVLENGVSLSTKLVQYFAGLILMVETGEVYALLTEENLSDIND	566
Query	507	WKIFDQVNEERELKQMLPKESYVLPIDYALSGLAMV-CTADKSLSRPILNIVSL	664
Subject	517	+E+ + + LK+4+D + E + P + L + + + C R P + E I S IS ---KEDGQSGLQVDFPMSEFNPSELISLPMYVFLDCLNKNPADRPAMEISQSL	622
Query	565	S 565	
Subject	623	S 623	

>ref|XP_002269408.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=638



GENE ID: 100242712 LOC100242712 | hypothetical protein LOC100242712
[Vitis vinifera]

Score = 263 bits (673), Expect = 4e-68, Method: Compositional matrix adjust.
Identities = 176/574 (30%), Positives = 293/574 (51%), Gaps = 66/574 (11%)

Query 47 SCETVYTYIAQSSPNFLSTNINISIFDTPSLAIARASLENPMDDKLKVDQLLVPTCTGGT 106
GCATGTTAATA P A L S L T A T G A + + P A A A A A + K A V A V F V C C A

[illegible]

[illegible]

```
>ref|XP_002327712.1|  predicted protein [Populus trichocarpa]
gb|EEE75190.1|  predicted protein [Populus trichocarpa]
Length=630
```

GENE ID: 7464252 POPTRDRAFT_796841 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 258 bits (658), Expect = 2e-66, Method: Compositional matrix adjust.
Identities = 181/588 (30%), Positives = 297/588 (50%), Gaps = 90/588 (15%)

[illegible]

>ref|XP_002310777.1| predicted protein [Populus trichocarpa]

gb|EEE91227.1|  predicted protein [Populus trichocarpa]

length=643

GENE ID: 7477999 POPTRDRAFT_563086 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 254 bits (649), Expect = 2e-65, Method: Compositional matrix adjust.
Identities = 280/586 (30%), Positives = 289/586 (49%), Gaps = 84/586 (14%)

[illegible]

```

Query 267 LLVYVYCLMKMT-----LNRSASSAETADKLLSGVSGVSKPTMYETD 309
          ++ ++ K K K INR E LL V +Y +
Sbjct 289 IIFMLFRSKKQPGPIIVSQSFARSKPLNKLID--EEDQDLLESVYIAQSIKYVNYE 346

Query 310 AIMEATMNLSEQCKIGESYKANIIEGKVLAVKRFEDVTEELIKLVQNHGILVKMGVS 369
          + AT N S + + + + + I G A + + + + + DV + + + + + L K + NH NL + + L GV
Sbjct 347 DLKAATNDSFPMIKSGVFGGLNGLFANLKNNGQVSKETILLKRNENLILGLVNC 406

Query 370 SSDNGCNFYVYVYAEKNSLDLEWFSKSCSDTNSRASLTWCQRISMAVDVAMGLQYHHER 429
          NDC+ + + VYVYA NG L + + + + + + SN L W QRI + A DVA GI Y + H
Sbjct 407 F+NDGHWLYVYVYAAANGSPISDWIYV-----SSNEGFLKWTQRILQIATDVATGLNLYHSP 460


Query 430 A+YPRIVHRDITSSNILLDSNFKAKIANFSMARTITNP-----MMP----- 469
          YP VHRDI SSNILLD + AKIANFS+AR+ P M P
Sbjct 461 TNYPR-VHRDILKSSNILLDKDLRAKIANFSLARSSTDGPEGEFALTRHIVCFKGMHPEYL 519

Query 470 -----KIDVAFGCVLIELLIGCRK--AMTTKNGEVMVLAKMDIK--ITDQENREERKL 519
          K+V+ATGCV+ + + + + + + A+ +EM E+ D+ + +E EE L
Sbjct 520 ENNGICTILQDVAFGLIELIMTGKEVAALYREKRENL-----SDVINGVLSEEGCLRESL 575

Query 520 KKKMDPKLESYPIIDVALSLASLVNCTADKSLRPTIAEIVLSL 565
          + + DP + + + YP A + + L + C RP + EIV SLIS
Sbjct 576 BQLIDPSMQNGYPSGLVIMVRLIDSLCKNNFAGRPAMDEIVQSLIS 621

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>ref|XP_002281880.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=622

GENE ID: 100248852 LOC100248852 | hypothetical protein LOC100248852
[Vitis vinifera]

Score = 253 bits (647), Expect = 4e-65, Method: Compositional matrix adjust.
Identities = 178/567 (31%), Positives = 289/567 (50%), Gaps = 62/567 (10%)

Query 47 SCETVYTYIAQSPNFIISLITNISINFDTPSLSTARASNLPMDDKLVKDOVLIVPVTCCT 106
          SC + + + + + P + S + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 54 SCQAFILTKRSGVPTKQVSTPTSMILMSSNGSEALINMVKTITLITVPTFGKEVY+VFNKGC 111

Query 107 GNRSPANIYEINGDSFYIV-ATTSYENLNNRWAVMDLNVLSFNKFLIGICGVPLFLC 165
          G AS + + + + + S YF+ + + L+ + + M N S L G + + + + + EL C
Sbjct 112 GQYQYQANTTTHIQDQWQYTYIIQNNYIYQGLSTCDSILNRNR+SEFSLSPGLGLHVLPLC 170

Query 166 KCPKRNQLDKEIKYLITYVKKPGDNVSLVSDKFGASPEDIMSENNY--GNFTAANNLEV 223
          C + + + Q + KYL+TY DN + + + F S + I N + N T +
Sbjct 171 ACHTEHQAENOTKYLITYSVSWEDNFTPIGERFNRSAKSIADANGLISEENPTIFFPTTI 230

Query 224 LIPVTRLPVLAR-----SPSDGRKGIRLPVITIGISLCTLL--VVVLV 264
          L P + + + + + R + + + + + G I + G C LL + + + + +
Sbjct 231 LPLKTEPLSRGQTKTHATQVLDPPPTTS DSGSSRSKRRIYLGACGIAACGLSPGVIFS 290

Query 265 AVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGVSKPTMYETDAIMEATMNLSEQCKI 324
          V L Y K K + + + + + LL + + + + + P + + + + + + AT N S + + I
Sbjct 291 IVFLPKKRSKRVVPVFGKTKSVLPEDLLVEIASVDVFPVKFPEFKLKKATGNFSSKRI 350

Query 325 GESVYKANIEGKVLAVKRFEDVTEELIKLVQNHGILVKMGVSSDNGCPT-VYVYA 383
          V + A + + + + + AVK+ K D + + EE+ IL K + NH NL + K L GV + G + CF + + + + +
Sbjct 351 KCV+PRAIGREIVAYKNSVDISSEWVLMKLNHGLKILKHCY--KNGSCYLVITYEM 408

Query 384 ENGSLDEWLFKSCSDTNSRASLTWCQRISMAVDVAMGLQYHHERAYPRIVHRDITSEN 443
          ENGSL DWE + S S S + W + RI + + + + + A GL Y + H P VHR + I SSN
Sbjct 409 ENGSLREWLHKS-----SNRSGWSKRIQIALDVANGLEYIHNTPKPAYVHKHKSIN 462



Query 444 ILLDGNFKAKIANFSMART-----FTNE-----MMPKIDVAFG 477
          ILL N + AKIANFS+ART + P + + + + + + + + + + + + + + + + +
Sbjct 463 ILLTANLRAKIANFSLARTAVKGAETHALNMLVVGTRGMYAPEYIEAGSITPKVDVAFG 522

Query 478 VVLELLEGRKAMTTKNGEVMVLAKMDIKITDQENREERKLKMDKNDKLESYPIIDVAL 537
          VV + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 523 VVMLELITGKDAVII--QNEEVLLEAMISIMER-GNAEIELGHFLDCLLGNNGGIESAT 580

Query 538 SLASLVNCTADKSLRPTIAEIVLSL 564
          + A L + + C RP + + + E + V + L
Sbjct 581 RIARLSIACTLKDQARRSPGMEGVSTL 607

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>ref|XP_002509540.1|  ATP binding protein, putative [Ricinus communis]
gb|EEF50927.1|  ATP binding protein, putative [Ricinus communis]
Length=681

GENE ID: 8271475 RCOM_1677900 | ATP binding protein, putative
[Ricinus communis]

Score = 253 bits (647), Expect = 4e-65, Method: Compositional matrix adjust.
Identities = 201/621 (32%), Positives = 299/621 (48%), Gaps = 104/621 (16%)

Query 44 SPSPCEYTYTYIAQSPNFIISLITNISINFDTPSLSTARASNLPMDDKLVKDOVLIVPVTC 103
          S C + T + + + + + F SL + K + S + + IA A + + + + + + L KDQ LL + P + C
Sbjct 49 SQDCKTFAL-LSITNGYSSLSKLSFYLQENRFVIAEANGFSADTEFLPKDQPLILIDC 107

Query 104 GCTGRNFSANIYEINGDSFYVATTSYENLNNRWAVMDLNVLSFNKFLIGICGVPLFLC 163
          T C Q N + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 108 KCGNCFNRAEYVTKTITIGENPFYGLAE-SLEGLTCKAIQENNLGVSPNMLADKARLVEL 166

Query 164 FCKPCKRNQLDKEIKYLITYVKKPGDNVSLVSDKFGASPEDIMSENNY--GNFTAANNLEV 222
          C CPS + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 167 RCACPSSSQVTLATREFLSYVSEGGDTISNIAIKENTTFEALISANNRSIANEFENILV 226

Query 223 -----VILVTRLPVLAR-----RSP-SDGRKGIRLPVITIGISLCTLLV- 261
          + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 227 LASLLIPNLRPALGSLAKRPEPNPSFPRESSI--FVINPHKKKSMIGVIAVTCGVV 284

Query 262 -----LVLLAVLVYVYCLMKMTLNRS-----SASSAETADKLLS--GVSGVSKPTM 305
          + V A L + V + K + L + + + + + S S + + K + S C + + + + +
Sbjct 285 GATIAIVAAFLVLQKLLKKKQNLKSDGDPQLQQLSLVSRVTTSEKRVSPFEGSQDLDNQI 344

Query 306 -----YETDAIMEATMNLSEQCKIGESYKANIIEGKVLAVKRFEDVTEELIKLVQNH 352

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Sbjct 345      Y + + + AT + S I SVY + GK LA+KR E + ++ 404
DTTPNRKRVLENYNYVEELRKATETDPSSSLIDGVSYYGRINGKNAIKRTKSETISKID

Query 353      ILQKVN-----HGNLKMVGSSNDNGCVFVVEYEAAGSLDEWL-----FSKSCSD 399
N H N++L+G + F+V+EYA+NGSL+WL F SC
Sbjct 405      FSHFQNAITHHPNIRLLKLTCLSEGSDFLVFVEYAKNGSLKDWLHGGLAMKNQFIASC-- 462

Query 400      TSNRSASLTWCQRISMMAVDMVAMGLQYMHEAYPRIVHRDITSNLLDSSFKAKIANFSM 459
LTM QR+ + DVA+ LQYMH P VHR+ S NI LD P AKI NP M
Sbjct 463      ---YCLTNNQLKLCLEAVAGLYMHMMFSPYVHRNKSINFLDEEFPNAKIGNPM 518






Query 460      ARTF-----TNF-----MMKPIDVAFGCVLLILLGRKAMT 491
AS TNP + P ID+FAFGVLE+L+G++ +
Sbjct 519      ARCIEGDTQTRITSTNPSMSLOYLAPEYIHQITVSPCIDFAFGVLLVLSOKRPT 578

Query 492      TKEV-GEVVMWMDIKWIKFDQENREERLKKWMDPKLESYYPIDYALSLASLVNCTADK 50
N GE L + K EN E L+WM D L Y D A++LA+LA+C ++
Sbjct 579      RPNKGEEENLSEKMSILSSENAGE-LAEEMDMLAGENTSFDPTAVLIANRASCVEE 637

Query 551      SLRSPTIADIVLSLSLITQSS 571
RP E+V LS L S
Sbjct 638      PBLRPNAGILVEKLSILVER 658

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>ref|NP_001058110.1|  Os06g0625200 [Oryza sativa Japonica Group]
dbj|BAD35689.1|  receptor protein kinase-like [Oryza sativa Japonica Group]
dbj|BAD37734.1|  receptor protein kinase-like [Oryza sativa Japonica Group]
gb|Z20024.1|  Os06g0625200 [Oryza sativa Japonica Group]
gb|KAZ27689.1|  hypothetical protein OsJ_22029 [Oryza sativa Japonica Group]
Length=630

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GENE ID: 4341567 Os06g0625200 | Os06g0625200 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

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Score = 251 bits (640), Expect = 3e-64, Method: Compositional matrix adjust.
Identities = 170/578 (29%), Positives = 297/578 (51%), Gaps = 86/578 (14%)

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Query 47      SCTETVYITAGSPNFIISNTNISITDTSPLSIARASNLPMDDKLKQVLLVPTCGT 106
E + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 56      SCTAYLTFRSDPP-----LSVAYLLNATPSAVAANSVPLAVSPVDGTLQVLPVFCSC- 109

Query 107      GNRSPA-----NISYEINGQDSFYFVATTSYENLTKWRVMDLNPVLSPNKLPICIGVQVP 162
NR+ N +Y I + D+P+ A + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 110      -NRATQYQYQNTTAYIQELDTFFLIANNITFQGLTTYQSIIANPASEMSPVINGPLAV 168

Query 163      LPCKCPKSKNQDKIKYILTYTVVKPQCNVLSVSKFGASPEDISSENNYQNFTANNPL 222
L C C P N Q N + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 169      LACACPSATT--GRINLLTYVQEGSNVTSIARFNSTHGDLVAANT----- 214

Query 223      VLIPTVRLP-----VLARSPDGRK-----GRLPVLIGISIGCTLLVLVL 258
+L+P+ P + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 215      LLVLVLPHRPSRVRVLIANTTITSTTPESQKPYVBSFSCNGLAGLIGVCGVSAWAVAL 274

Query 265      AVLLVYVYCKMLKTLNRSASAEATADKLISGVSGVSKPTMYTTDAIMEATNLSGECKR 324
AV L+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 275      AVTLWRRRRRPFVGDSSGMARET--FLVAAVGVAETLAATYADITETATGAFAERRRV 332

Query 325      --GEVYKANTEGKLVAKRKF-----EDVTEELIKLVNHNGLVLMGVSSNDNGCVFV 379
G SVY+ A T G+ ANR+ DV E+ L +VNH LVH G+ + + + + + + + + + + + + + +
Sbjct 333      AAGSSVYRVINGEAFVAKRVAAGDGVGEVLDVLRVNHSGVLRLGLCANGD-DTYIL 391

Query 380      YEYAGNSGLDEWLFSKSDCTSNRSASLTWCQRISMMAVDMVAMGLQYMHEAYPRIVHRDI 439
E+AEAG+L EWL S + + R L W QR+ + +DVA GL Y+H P VH++ +
Sbjct 392      LEFAENGALSEWLHPGSA--ACLARVLGWKQVRLVALDVAGGINYLHFTNPPTVYHNL 449

Query 440      TSNLLDSSFKAKIANFSM-----ARTFTNP-----NM 508
S N H+P N A K A K + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 450      NBNGLVLDANLRAKIVLSLGEFAVARAVAAAGDSIALMTHRVVGLAEPYLEHGLIS 469

Query 469      PKIDVFAFGCVLLILLTRK-KAMT+TKENGVEVVMWMDIKWIKFDQENREERLKKWMDPKL 527
PR+DVF+FGV+ +ELL+G+ A T + +G+ +LW+ + D + + + + + + + + + + + + + +
Sbjct 510      PKLDVSPFGVQLLELSGKTAAFPVTDGQGNMLLQAAADGLVDG-DGAWFKLRAFMPOQL 568

Query 528      ESYYPIDYALSLASLVNCTADKLSRPTIADIVLSLS 565
+ +YPI A + +A+LAV C A + +RP+ E + + + + + + + + + + + + + + + + +
Sbjct 569      QSHYPIGVASAAVALAVRCVAREPARPASMEEVPTLS 606


```

```

>ref|XP_002307830.1|  predicted protein [Populus trichocarpa]

```

```

gb|EEE94826.1|  predicted protein [Populus trichocarpa]
Length=639

```

```

GENE ID: 7479122 POPTDRRAFT_862283 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

```

```

Score = 248 bits (632), Expect = 2e-63, Method: Compositional matrix adjust.
Identities = 170/589 (28%), Positives = 295/589 (50%), Gaps = 82/589 (13%)

```

```

Query 47      SCTETVYITAGSPNFIISNTNISITDTSPLSIARASNLPMDDKLKQVLLVPTCGT 104
SC++Y+T+ + P + S E+ + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 58      SCQSLYTFRSMPP-YNSVPLIAYLLGVQPSATRIASINNLSSDTATIPNTQGVVFNCS 116

Query 105      CTGNRSFA-NISYEI-NQGDSEFYFVATTSYENLTKWRVMDLNPVLSPNKLPICIGVQVP 162
C + + N +Y++ + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 117      CYARQYQYQNTYQLKRSSETYSVANNTYQGLITQCSIMSNQNPYGDNR-LSIGITLQIP 175

Query 163      LPCKCPKSKNQDKIKYILTYTVVKPQCNVLSVSKFGASPEDISSENNYQNFTANNPL 222
L C C P N Q N + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 176      LACACPSNANSGINHLTYVYVWGSISLQGLPQVOKQVRLVDANKLSSNITFFPT 235

Query 223      VLIPTVRLP-----LARSFSDGRKGI-RLPVLIGISIGCTLLVLVLVL 267
+L+P+ P + +P+ C + +H+ HC L+L+ A
Sbjct 236      ILVLPLEPTEKTIEQPSAAPPAPSPQPNVSVGGSSDHKALVGVGVLGAAPFLILLFAF 295

```

```

Query 268 LVVVYCLMKTLNRSASSARTADKLLSGVSGYVSKP-----TMY 306
              K + + S+E + L S + + E TTY
Sbjct 296 GFLFMRKSGKQKQKPVSRSE-PTTLRSTVDTVLVPSNNKWSLSSHDARYAIESLTVY 354
              K + + S + + + SVY+ + +G AVK K DV+ E+ IL+ +NB N++IL
Query 307 ETDADMEATNNLSQEQKIGSVYKANIEGKVLAVKFKFVTEELKLOKVVNBNLAKIM 366
              + + AT + + SVY+ + +G AVK K DV+ E+ IL+ +NB N++IL
Sbjct 355 KYEDLQVATQYPAQANLIGSVYRGSFGDTAAVKVKVDSSINILKMNHNSVRLIS 414
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Query 367 GVSSDNGCNGCVVYVYEAENGSLDEMLFSKSCSDTNSRASLTWCQRISMAVDVAMGLQYM 426
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Sbjct 415 GFCL-HEGNTLVYETAAGNSLTDWLS- ----NNIYRILAWQRVRIATYVADALNTL 467
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Query 427 HEHAYPRVIRHDTSSNILLDGNFKAKIANTSMARTFNP----- 466
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Sbjct 468 HAYTFPSYIKHNKLNILLDANLAKAVANFGLARTLENGQDGLQLTRHVCTQCYLAP 527
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Query 467 -----MMKPIDVFAFGVLIETLTGRKAMTT--KENGEVVMWKMDKIPDQENRE 516
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Sbjct 528 EYIENGVTPLDVFAGVVMLELLSGKEAAATAIDRIAGD-DLLSVIMIRVL-EGDINVR 585
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Query 517 ERAKKMDPKLESYYPIDVALSIASLAVNCTADKSLRPTIAEVLISLS 565
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Sbjct 586 EKASLAFDCLRDDEYPLDIAFSMAQLAKSCVEHDLNTRPSMPQVPMMLIS 634
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+

```

>emb|CAO02961.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=131


Score = 240 bits (613), Expect = 4e-61, Method: Composition-based stats.
Identities = 111/130 (85%), Positives = 121/130 (93%), Gaps = 0/130 (0%)

```

Query 412 RISMAVDVAMGLQYMEHAYPRVIRHDTSSNILLDGNFKAKIANTSMARTFNPMMFKI 471
              RI++A+DVA+GLQYMEHAYPRVIRHDTSSNILL DGNFKAKIANT SMART FN MMFKI
Sbjct 1 RITIAMDAIGLQYMEHAYPRIIRHDTSSNILLDGNFKAKIANTSMARTFNPMMFKI 60
              RITIAMDAIGLQYMEHAYPRIIRHDTSSNILL DGNFKAKIANT SMART FN MMFKI
Query 472 DVFAFGVLIETLTGRKAMTTKNGEVMVLMKMDKIPDQENREERLRKMDPKLESYY 531
              DVFAFGVLIETLTGRKAMTTKNGEVMVLMKMDKIPDQENREERLRKMDPKLESYY
Sbjct 61 DVFAFGVLIETLTGRKAMTTKNGEVMVLMKMDKIPDQENREERLRKMDPKLESYY 120
              DVFAFGVLIETLTGRKAMTTKNGEVMVLMKMDKIPDQENREERLRKMDPKLESYY
Query 532 PIDVALSIAS 541
              PID VALSIAS
Sbjct 121 PIDVALSIAS 130
              PID VALSIAS

```

>ref|XP_002300098.1|  predicted protein [Populus trichocarpa]

gb|EE84903.1|  predicted protein [Populus trichocarpa]
Length=680

GENE ID: 746712 POPTDRAFT_641782 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 238 bits (607), Expect = 2e-60, Method: Compositional matrix adjust.
Identities = 196/650 (30%), Positives = 304/650 (46%), Gaps = 104/650 (16%)

```

Query 14 LILCVMLFSTNIVA-QSQGNRTNFCPSDS-PPSCETVYTYIAQSNFSLTNSINIF 71
              +CL+ + N+ + Q+ + + C S+ + C+T S P SL+N+S
Sbjct 19 LILCVLSALQNLSCQTTSPDASGYHCNSNGLQDQCKTFAI-LHTSYFSLNSLSFYL 77
              LILCVLSALQNLSCQTTSPDASGYHCNSNGLQDQCKTFAI-LHTSYFSLNSLSFYL
Query 72 DTSPLSIARASNLREMDKVLKQDVLIVPTCGCTGNRFSANISYEINQDSFYFVATPS 131
              IA + + L KQ LL+P+ C C G A + + +G+SFY + + S
Sbjct 78 GLDRFVIAATNGFSANTEFLPKDQELLIPIDCKCNGGFFQALVTKTTIKGEFSYI-SKS 136
              IA + + L KQ LL+P+ C C G A + + +G+SFY + + S
Query 132 YENLTNMRVADNPVLSNPKLPIGIVQVFFLECKCPKSNQDLKEIKYLITVWPKGDNV 191
              E L L + + + NP +B + + +G+ PL C CPS + + +L + + +D +
Sbjct 137 LEGLTTCALISEKPNISPEINLNGVQLQVFLKACPSSTEVILATRLILSVFSAQDTT 196
              E L L + + + NP +B + + +G+ PL C CPS + + +L + + +D +
Query 192 SLVSKQSGASPEDIMSEN-----YQGNFT----AANLPLV-LP 226
              S + + KF +E I S NN G T A N P L P
Sbjct 197 SNLAIKENTTPAITSANNRSLTTFKFTSLVPLTSLILPLGCKPTLGLAKNPNELHLP 256
              S + + KF +E I S NN G T A N P L P
Query 227 VTRLPVLARSPSDGRKGGRILPVIIGISLGLCTLLVLVLVLLVYVYCLEMKTNRSASSA 286
              + LPV+ +D R R + V I + + + +A + + K K + +
Sbjct 257 ASSEPLV--NPKHKKRKMGRGVYIATVAGVGSIAIAAALVILQKKRQVLSKEADT 314
              + LPV+ +D R R + V I + + + +A + + K K + +
Query 287 E-----PAKLLS-----GVSGYVSKPT-----MYETDADMEATNNLSQEQK 323
              E + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 315 ELQQLSLSVRTTSDKKVSPDSQNFQSDITDTTPGKVFVETTYVEELKRAEDENSSNQ 374
              E + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Query 324 IGSVYKANIIEGKVLAVKFKFVDVTE--ELKILQV--NHNGLVLMGVSSDNGCNGFV 379
              I SVY + GK LA+KR + + EL + Q +H N+++++G + +P+V
Sbjct 375 IGSVYHGLRNGKLAIRKQVQPTISKVLGLGQDATHHFNIRVVGTCLESGPDSFLV 434
              I SVY + GK LA+KR + + EL + Q +H N+++++G + +P+V
Query 380 YEYANGSLDEML-----FSKSCSDTNSRASLTWCQRISMAVDVAMGLQYMEHAY 430
              +EYANGSS+WL + + SC LTR QR+ + +DVA+ LQYMH
Sbjct 435 YEYANGSLDEML-----FSKSCSDTNSRASLTWCQRISMAVDVAMGLQYMEHAY 488
              +EYANGSS+WL + + SC LTR QR+ + +DVA+ LQYMH
Query 431 YPRVIRHDTSSNILLDGNFKAKIANTSMARTFNP-----TNP-----MMK-- 470
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Sbjct 489 HPSYVHRNKSRNIFLOEENFNAKINGMGAGVEDDTEKDPDNSTNPASNSLGLYLAFAEH 540
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Query 471 -----IDVFAFGVLIETLTGRKAMTT--KENGEVVMWKMDKIPDQENREERLRK 521
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Sbjct 549 QGVVSSSTDFSGVVMLEVLSSGQPTIRPNUNGEGSILMSKRSKIL-LISEADE-LRE 606
              + +GN + +VYETA+NGSL +WL S +N L W QR+ +A DVA L Y+
Query 522 KMDPKLESYYPIDVALSIASLAVNCTADKSLRPTIAEVLISLSLTQPS 571
              KMD + Y P A +LH+V+ C+ + RPT EIV L L L + S
Sbjct 607 WIDSAMGSEYSPDRAATLANIARACTREKPSLRFTSGEIVKILRLVKEES 656
              KMD + Y P A +LH+V+ C+ + RPT EIV L L L + S

```

>ref|NP_566689.2|  CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein7 transmembrane receptor protein kinase [Arabidopsis thaliana]

dbj|BAF92788.1|  chitin elicitor receptor kinase 1 [Arabidopsis thaliana]

Length=617

GENE ID: 821717 CERK1 | CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/
receptor signaling protein/transmembrane receptor protein kinase
[Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 236 bits (602), Expect = 8e-60, Method: Compositional matrix adjust.
Identities = 163/535 (30%), Positives = 270/535 (50%), Gaps = 74/535 (13%)

```
Query 89  DRKLVKQVILVPPVTCGCT-GNRBFANI SYEINQDGSFYVATTSYENLTNWRVMDINLV 147
D++ +LVP C C G+ N SY + Q D++ VA ++Y NLZ ++ NP
Sbjct 77  DRKMGSRVILVPPPCCGQDFLGNFSYVQRGDTYERVAISNIANTLTMSLGQARNFF 136

Query 148  LSPNKLPIQIQVVPFLFCCKPSKNQLDKEKLYITLVKMGQDNRVILVSDKFGASPEDINS 207
+ N + + + C C + + + K+ + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 137  PATN-IPISATINLVVNCSDGDS-VSKDQGLFVTVPLRPFDSISARSSGVSA-DIIQ 193

Query 208  ENNYQNFTAAANNL---VLIIPVTRLPVARSFDRGKRGILFVIGISGLCTILVILV 264
N G NP + N + P P P P S DG G VI GI + G + +L+ +
Sbjct 194  RYNGPWFNFSNGVIVYVGRDNGPAGFPFSSSKQDGVGAG---VIAGIVIGVAILLI 249

Query 265  AVLLVYVVC-----LKMKTINRGAASAEATDKLLSGVSGVYS---KPM 305
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 250  LFTVYVYAYRKNKSKDGSFSSSILPLSKADIASSTSLQSGILGAGVSRGIAAISVDKSGVE 309

Query 306  YETDAIMEATNLSQCKICE-----SVYKANIEGKVLAVKRFREDVTE-----ELKILQKV 357
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 310  FSLEELAKATDNFNLFRKIGQGGFCVAYAEIRGEKAAIKMDMEASKQFLAEKLVLRV 369

Query 358  NHGNLVKMGVSDNDGNCQFVYVEAENGSLDEWLFSEKSCSDTNSRASLTWCQRISMAV 417
+H NIW+L+G + G+ P+VVEY ENG+L+L + + R L W +R+ +A+
Sbjct 370  HHVNLVRLIGYVCE--GSLFLVVEYENGVLQGLHGL-----SGREPLFWTRKQVIAL 420

Query 418  DVAMGLQVMEHAYPRVHRDITSSNILLDSNFKAIANFMSAR----- 461
D A GL+ + + + + P VIRD I SNI+LD PAK+AF + + +
Sbjct 421  DSAAGLSEYIHEHTVYVYVHRDIKSIANLIDQKFAKAVADFGLTKLTVGGSGATGAMGTF 480

Query 462  -----TFINPMKQKIDVAFGVVLIELLTGRKAMTKENGVEVMWKDKIKFIQ---E 512
T + K+D+AFGVWL EL+ + + + + E V + + + + + + + + + + + + + + + + +
Sbjct 481  GYMAPETVYGEVSAKVYVYAGVVLVYELISAKGAVVRMT---EAVGEFRGLGVCFEESFKE 538

Query 513  ENREERLKKWMDPKLESYIPIDYALSIALAVNCATDKSLRPRTAIVLSLSLL 567
++EE L+K+DP+L YP D +A L CT + + + R+ + + + + + + + + + + + + + + + +
Sbjct 539  TDKEAEARKIIDPRIGDSYFSDSVYKMAELGKACTQENAGLRFPMRYIVVALSTL 593
```

>emb|CB140054.3| unnamed protein product [Vitis vinifera]

Length=672

Score = 234 bits (598), Expect = 2e-59, Method: Compositional matrix adjust.
Identities = 181/631 (28%), Positives = 297/631 (47%), Gaps = 69/631 (10%)

```
Query 14  ILCLVIMLFSNINVAQSQDNRNFSQPSD-SPPSCETVTVYIAQSPNLSLTNINISFD 72
IL V L + + + + + + + C + S C T+ S + SL N+S
Sbjct 17  ILVFPVTLQGLSLCETSRRDASGYCNGSGQKCGTQFALLATNS-YISSLFLNLSFYLG 75

Query 73  TSPSLTARANSLEPMQDVKDQVILVPPVTCGCTGNRSFANI SYEINQDGSFYVATTBY 132
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 76  IDRELIAGFNSGASDELPIELPILLIPIECKAGGFAELTKTTTIGSESFTGAE-SL 134

Query 133  ENLNVRAVMDLNVPVLSNPKLPIQIQVVPFLFCCKPSKNQLDKEKLYITLVKMGQDNRV 192
E I+ +A+ + NP + P L + + + + PL C CPS +L+ +E K L+ + + + + + + + + + + +
Sbjct 135  EQLTCKATIRERNPSIQPGWADKRVLLILPLRCACPSSESLIQLTKLLSYVPSGDTVP 194

Query 193  LVSDKFGASPEDIMSENNY-QNFTAAANLP-VLIIPVTRLPVARSFDRGKRGILFV 249
++ KF + E I+S NN G + P + + P T +PV+ + P + + + + + + + + + + + + + + + + +
Sbjct 195  SLAFKFTPTSEATISANKRGATRLRLGLAPPNLGLPATSIPVT--NPHKRTKMKWIGV 252

Query 250  I I---GISGLTLLVILVILVILVY-----VYCLRMKTINRGAASAEAT 289
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 251  YIAVSGVAVGASV-AIAAALVIVHWRKKQNAKMGDVELQGLSVRTTEKKVSEFGS 311

Query 290  DKLLSGVSGVYSKPTMYETDAIME---ATMNLSEQCKIGESVYKANIEGKVLAVKRFKED 346
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 312  QDPIDQITIDSPHKIVETVYTMLELRKATDFNNSNLLIGSVFHRGLNKNLAIKHTPE 371


Query 347  VTE-ELKILQKV--NHGNLVKMGVSDNDGNCQFVYVEAENGSLDEWLFSEKSCSDT--- 400
+ + G V L + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 372  AISKTEFGLFDDAHHEHNINMLLGTCLNPSGDSYLIIFYANSLKLDWHLGGLAMKSGF 439

Query 401  -SNSRASLTWCQRISMAVDVAMGLQVMEHAYPRVHRDITSSNILLDSNFKAIANFMS 451
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 402  IASCYCLTNQRLRLCGLDAMALQYMRHIMHPCYVHRNKSNIPLDDEEFNAKNGFM 491

Query 460  ARTFTNP-----MMKPIDVAFGVVLIELLTGRKAMTK 493
AR F + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 492  ARCFEDDAEDSQPYSTASWSKGLAPEYLRQGISPTLQIFAYGVVLVLSGKTPITRA 551

Query 494  EN---GEVVMWKDKIKFIQDEENREERLKKWMDPKLESYIPIDYALSIALAVNCATDKS 551
+ + G V L + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct 552  DDKGSGVWLPEKIKSLIGSENT---ELRDMWMSALGENTSDYDAITLAAVLAVCTDENP 609

Query 552  LSRPTAIVLSLSLLTQSPATLERLSLTSS 582
SRP+ EIV LS L + P + S+ S
Sbjct 610  CSRPSAGEIVKLSRLVQLPEGEQFICES 640
```

>ref|XP_002263070.1|  PREDICTED: hypothetical protein [Vitis vinifera]

Length=675

GENE ID: 100264694 LOC100264694 | hypothetical protein LOC100264694
[Vitis vinifera] (10 or fewer PubMed links)

Score = 233 bits (595), Expect = 4e-59, Method: Compositional matrix adjust.
Identities = 185/652 (28%), Positives = 298/652 (45%), Gaps = 89/652 (13%)

```
Query 14  ILCLVIMLFSNINVAQSQDNRNFSQPSD-SPPSCETVTVYIAQSPNLSLTNINISFD 72
```

[illegible]

Select All Get selected sequences Distance tree of results Multiple alignment

APPENDIX C

Claim	Type	Depends from	%ID	AA SEQ ID	NA SEQ ID
59.	AA	-	80 AA	8 15 31 32 40 48	-
60.	AA	-	80 AA	24 25	-
61.	AA	59	100 AA	8 15 31 32 40 48	-
62.	AA	60	100 AA	24 25	-
63.	AA-combo	59 + seq	80/80 AA	8 15 31 32 40 48/ 24 25 52 54	-
64.	AA-combo	61(59)	100/100 AA	8 15 31 32 40 48/ 24 25 52 54	-
65.	NA	59	80 AA	ENC 80%[8 15 31 32 40 48]	-
66.	NA	60	80 AA	ENC80%[24 25]	-
67.	NA	65 (59)	100 NA	[encode 80% 8 15 31 32 40 48]	6 7 11 12 30 39 47
68.	NA	66 (60)	100 NA	[encode 80% 24 25]	21 22 23
69.	Tg cell NA	59	80 AA	[encode 80% 8 15 31 32 40 48]	-
70.	Tg cell NA	69(59)	100 AA	[encode 100% 8 15 31 32 40 48]	-
71.	Tg cell NA	69(59)	100 NA	[encode 80% 8 15 31 32 40 48]	6 7 11 12 30 39 47
72.	Tg cell NA	60	80 AA	ENC80%[24 25]	-
73.	Tg cell NA	72(60)	100 AA	ENC100%[24 25]	-
74.	Tg cell NA	72(60)	100 NA	ENC 80%[24 25]	21 22 23
75.	Tg cell NA	63(59)	80/80 AA	[enc 8 15 31 32 40 48/ 24 25 52 54]	-
76.	Tg cell NA	63(59)	100/100 AA	[enc 8 15 31 32 40 48/ 24 25 52 54]	-
77.	plant cell	Xxx			
78.	plant cell	Xxx			
79.	plant cell	Xxx			
80.	plant cell	Xxx			
81.	plant cell	Xxx			
82.	plant cell	Xxx			
83.	plant cell	Xxx			
84.	plant cell	Xxx			
85.	method	59	80 AA	8 15 31 32 40 48	-
86.	method	85(59)	100 AA	8 15 31 32 40 48	-
87.	method	85(50)	100 NA	[encode 80% 8 15 31 32 40 48]	6 7 11 12 30 39 47
88.	method	60	80 AA	24 25	-
89.	method	88 (60)	100 AA	24 25	-
90.	method	88(60)	100 NA	[encodes 80% 24 25]	21 22 23
91.	method	85(59)	80/80 AA	[8 15 31 32 40 48/ 24 25 52 54]	-
92.	method	86 (85)(59)	100/100 AA	[8 15 31 32 40 48/ 24 25 52 54]	-
93.	method	91(85)(59)	100 NA	[encodes 80% 8 15 31 32 40 48/ 24 25 52 54]	6 7 11 12 30 39 47/ 21 22 23 51 53
94.	Method x	85(59)	80 AA	8 15 31 32 40 48	-
95.	Method x	88(60)	80 AA	24 25	-
96.	Method x	91(85)(59)	80/80 AA	[8 15 31 32 40 48/ 24 25 52 54]	-
97.	Method x	93(85)(59)	100 NA	[encodes 80% 8 15 31 32 40 48/ 24 25 52 54]	6 7 11 12 30 39 47/ 21 22 23 51 53
98.	Tg plant	59	80	8 15 31 32 40 48	-
99.	Tg plant	98(59)	100	8 15 31 32 40 48	-
100.	Tg plant	60	80	24 25	-
101.	Tg plant	100(60)	100	24 25	-
102.	Tg plant	63	80/80	8 15 31 32 40 48/ 24 25 52 54	-
103.	Tg plant	64	100/100	8 15 31 32 40 48/ 24 25 52 54	-

Claim	Type	Depends from	%ID	AA SEQ ID	NA SEQ ID
104.	Cereal	98(59)	80 AA	8 15 31 32 40 48	-
105.	Cereal	XXX			
106.	Cereal	100(60)	80 AA	24 25	-
107.	Cereal	XXX			
108.	Cereal	XXX			
109.	Cereal	XXX			
110.	Legume	98(59)	80 AA	8 15 31 32 40 48	-
111.	Legume	XXX			
112.	Legume	100(60)	80 AA	24 25	-
113.	Legume	XXX			
114.	Legume	XXX			
115.	Legume	XXX			
116.	Non-nod	98(59)	80 AA	8 15 31 32 40 48	-
117.	XXX				
118.	Non-nod	100(60)	80 AA	24 25	-
119.	XXX				
120.	XXX				
121.	XXX				
122.	AA	-	90 AA	52 54	-
123.	NA	122	90 AA	encodes 90%[52 54]	-
124.	Tg cell NA	122	90 AA	encodes 90%[52 54]	-
125.	Tg cell NA	124(122)	100 NA	Encodes 90% [52 54]	51 53
126.	Tg plant	122	90 AA	Encodes 90%[52 54]	-
127.	Tg plant	98(59)	80 AA	8	-
128.	Tg plant	98(59)	80 AA	15	-
129.	Tg plant	98(59)	80 AA	31	-
130.	Tg plant	98(59)	80 AA	32	-
131.	Tg plant	98(59)	80 AA	40	-
132.	Tg plant	98(59)	80 AA	48	-
133.	Tg plant	100(60)	80 AA	24	-
134.	Tg plant	59	100 AA	8	-
135.	Tg plant	59	100 AA	15	-
136.	Tg plant	59	100 AA	31	-
137.	Tg plant	59	100 AA	32	-
138.	Tg plant	59	100 AA	40	-
139.	Tg plant	59	100 AA	48	-
140.	Tg plant	60	100 AA	24	-
141.	Tg plant	122	100 AA	52	-

XXX=CANCELLED CLAIM

Claim 93 depends from claim 91

Claim 125 depends from claim 124